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APPLICATION FOR UNITED STATES LETTERS PATENT

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TITLE: ANGIOGENESIS ASSOCIATED PROTEINS AND NUCLEIC ACIDS ENCODING THE SAME

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ANGIOGENISIS ASSOCIATES PROTEINS, AND NUCLEIC ACIDS ENCODING THE SAME

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/191,134 filed 03/22/2000, which is incorporated herein by reference in its entirety.

BACKGROUND

Cities have roads and alleys, plants have xylem and phloem, and people have arteries, veins and lymphatics. Without these byways, the vertebrate animal cells would starve or drown in their metabolic refuse. Not only do blood vessels deliver food and oxygen and carry away metabolic wastes, but they also transport signaling substances that apprise cells of situations remote to them but to which they need to respond. Hormonal messages are a common signal.

All blood vessels are ensheathed by a basal lamina and a delicate monolayer of remarkably plastic endothelial cells lining the luminal walls. Depending on location and function, smooth muscle and connective tissue may also be present.

Not only do healthy cells depend on the blood resources transported by the circulatory system, but so, too, unwanted cells: tumorigenic and malignant cells. These cells colonize and proliferate if they are able to divert blood resources to themselves. Angiogenesis, the type of blood vessel formation where new vessels emerge from the proliferation of preexisting vessels (Risau, 1995; Risau and Flamme, 1995), is exploited not only by usual processes, such as in wound healing or myocardial infarction repair, but also by tumors themselves and in cancers, diabetic retinopathy, macular degeneration, psoriasis, and rheumatoid arthritis. Regardless of the process, whether pathological or usual physiological, endothelial cells mediate angiogenesis in a multi-step fashion: (1) endothelia receive an extracellular cue, (2) the signaled cells breach the basal lamina sheath, abetted by proteases they secrete, (3) the cells then migrate to the signal and proliferate, and finally, (4) the cells form a tube, a morphogenic event (Alberts *et al.*, 1994). The complexity of this process indicates complex changes in cellular physiology and morphology, gene expression, and signaling. Angiogenic accomplices that are cues

include basic fibroblast growth factors (bFGF), angiopoietins (such as ANG1) and various forms of vascular endothelial growth factor (VEGF).

The molecular events and the order in which they occur and the pathways that are required for this process are of fundamental importance to understand angiogenesis. *In vitro* models are useful for identifying alterations in gene expression that occur during angiogenesis. A particularly fruitful model systems involves the supspension in a three-dimensional type I collagen gel and various stimuli, such as phorbol myristate acetate (PMA), basic fibroblast growth factor (bFGF), and VEGF. The combination of the stimuli and the collagen gel results in the formation of a three-dimensional tubular network of endothelial cells with interconnecting lumenal structures. In this model, endothelial differentiation into tubelike structures is completely blocked by inhibitors of new mRNA or protein synthesis. Furthermore, the cells progress through differentiation in a coordinated and synchronized manner, thus optimizing the profile of gene expression (Kahn *et al.*, 2000; Yang *et al.*, 1999).

Tumor cells exploit angiogenesis to facilitate tumor growth. Controlling angiogenesis, by controlling the activity or expression of genes and proteins associated with angiogenesis, provides a way to prevent tumor growth, or even destoy tumors.

SUMMARY

The invention is based in part upon the discovery of novel nucleic acid sequences encoding novel polypeptides. Nucleic acids encoding the polypeptides disclosed in the invention, and derivatives and fragments thereof, will hereinafter be collectively designated as "AAP" nucleic acid or polypeptide sequences. AAP, or angiogenesis associated polypeptides (AAP) comprises kelch-like polypeptide (KLP), human ortholog of mouse BAZF (hBAZF), hmt-elongation factor G (hEF-G), human ortholog of rat TRG (hTRG), human myosin X (hMX1) and its splice variant (hMX2), nuclear hormone receptor (NHR), and human mitochondrial protein (hMP).

The invention is based in part upon the discovery of novel nucleic acid sequences encoding novel polypeptides. Nucleic acids encoding the polypeptides disclosed in the invention, and derivatives and fragments thereof, will hereinafter be collectively designated as "AAP" nucleic acid or polypeptide sequences."

In a first aspect, the present invention is an isolated polypeptide having at least 80% sequence identity to the sequence SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, polynucleotides encoding the same, and antibodies that specifically bind the same.

In a second aspect, the present invention is an isolated polynucleotide having at least 80% sequence identity to the sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement thereof.

In a third aspect, the present invention is a transgenic non-human animal, having a disrupted *AAP* gene or a transgenic non-human animal expressing an exogenous polynucleotide having at least 80% sequence identity to the sequence SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of said polynucleotide.

In a fourth aspect, the present invention is a method of screening a sample for a mutation in an *AAP* gene.

In a fifth aspect, the present invention is a method of modulating angiogenesis comprising modulating the activity of at least one AAP polypeptide.

In a sixth aspect, the present invention is a method of increasing, as well as decreasing angiogenesis, comprising modulating the activity of at least one AAP polypeptide. Activity modulation of AAP polypeptides may be over-expressing or eliminating expression of the gene, or impairing a AAP polypeptide's function by contact with specific antagonists or agonists, such as antibodies or aptamers.

In a seventh aspect, the present invention is a method of treating various pathologies, including tumors, cancers, myocardial infarctions and the like.

In an eighth aspect, the present invention is a method of measuring a AAP transcriptional and translational up-regulation or down-regulation activity of a compound.

In a ninth aspect, the invention is a method of screening a tissue sample for tumorigenic potential.

In a tenth aspect, the invention is a method of determining the clinical stage of tumor which compares the expression of at least one AAP in a sample with expression of said at least one gene in control samples.

Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other

references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

DETAILED DESCRIPTION

A model of angiogenesis-the suspension of endothelial cells in type I collagen gels with various stimuli-was used to identify a molecular fingerprint or transcriptional profile of endothelial differentiation into tubelike structures, using amplification and an imaging approach called GeneCalling (Shimkets *et al.*, 1999). This method was previously shown to provide a comprehensive sampling of cDNA populations in conjunction with the sensitive detection of quantitative differences in mRNA abundance for both known and novel genes. Many differentially expressed cDNA fragments were found. The identification and differential expression of these gens was confirmed by a second independent method employing real-time quantitative polymerase chain reaction (PCR). Although some of the identified cDNA fragments were genes known to play some role in angiogenesis, many other differentially expressed genes were unexpected. The inventors have identified the unexpected genes and polypeptides that are expressed in response to this model of angiogenesis, collectively refered to as angiogenesis associated polypeptides (AAP). AAP are kelch-like polypeptide (KLP), human ortholog of mouse BAZF (hBAZF), hmt-elongation factor G (hEF-G), human ortholog of rat TRG (hTRG), human myosin X (hMX1) and its splice variant (hMX2), nuclear hormone receptor (NHR), and human mitochondrial protein (hMP).

Definitions

Unless defined otherwise, all technical and scientific terms have the same meaning as is commonly understood by one of skill in the art to which this invention belongs. The definitions below are presented for clarity. All patents and publications referred to herein are, unless noted otherwise, incorporated by reference in their entirety.

The recommendations of (Demerec *et al.*, 1966) where these are relevant to genetics are adapted herein. To distinguish between genes (and related nucleic acids) and the proteins that they encode, the abbreviations for genes are indicated by *italicized* (or

underlined) text while abbreviations for the proteins start with a capital letter and are not italicized. Thus, *AAP* or AAP refers to the nucleotide sequence that encodes AAP.

"Isolated," when referred to a molecule, refers to a molecule that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that interfere with diagnostic or therapeutic use.

"Container" is used broadly to mean any receptacle for holding material or reagent. Containers may be fabricated of glass, plastic, ceramic, metal, or any other material that can hold reagents. Acceptable materials will not react adversely with the contents.

1. *Nucleic acid-related definitions*

(a) *control sequences*

Control sequences are DNA sequences that enable the expression of an operably-linked coding sequence in a particular host organism. Prokaryotic control sequences include promoters, operator sequences, and ribosome binding sites. Eukaryotic cells utilize promoters, polyadenylation signals, and enhancers.

(b) *operably-linked*

Nucleic acid is operably-linked when it is placed into a functional relationship with another nucleic acid sequence. For example, a promoter or enhancer is operably-linked to a coding sequence if it affects the transcription of the sequence, or a ribosome-binding site is operably-linked to a coding sequence if positioned to facilitate translation. Generally, "operably-linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by conventional recombinant DNA methods.

(c) *isolated nucleic acids*

An isolated nucleic acid molecule is purified from the setting in which it is found in nature and is separated from at least one contaminant nucleic acid molecule. Isolated *AAP* molecules are distinguished from the specific *AAP* molecule, as it exists in cells. However, an isolated *AAP* molecule includes *AAP* molecules contained in cells that

ordinarily express an AAP where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

2. *Protein-related definitions*

(a) *purified polypeptide*

When the molecule is a purified polypeptide, the polypeptide will be purified (1) to obtain at least 15 residues of N-terminal or internal amino acid sequence using a sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or silver stain. Isolated polypeptides include those expressed heterologously in genetically-engineered cells or expressed *in vitro*, since at least one component of an AAP natural environment will not be present. Ordinarily, isolated polypeptides are prepared by at least one purification step.

(b) *active polypeptide*

An active AAP or AAP fragment retains a biological and/or an immunological activity of the native or naturally-occurring AAP. Immunological activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native AAP; biological activity refers to a function, either inhibitory or stimulatory, caused by a native AAP that excludes immunological activity. A biological activity of AAP includes, for example, modulating angiogenesis.

(c) *Abs*

Antibody may be single anti-AAP monoclonal Abs (including agonist, antagonist, and neutralizing Abs), anti-AAP antibody compositions with polyepitopic specificity, single chain anti-AAP Abs, and fragments of anti-AAP Abs. A "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous Abs, *i.e.*, the individual Abs comprising the population are identical except for naturally-occurring mutations that may be present in minor amounts

(d) *epitope tags*

An epitope tagged polypeptide refers to a chimeric polypeptide fused to a "tag polypeptide". Such tags provide epitopes against which Abs can be made or are available, but do not interfere with polypeptide activity. To reduce anti-tag antibody reactivity with endogenous epitopes, the tag polypeptide is preferably unique. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8

and 50 amino acid residues, preferably between 8 and 20 amino acid residues). Examples of epitope tag sequences include HA from *Influenza* A virus and FLAG.

The novel *AAP* of the invention include the nucleic acids whose sequences are provided in Tables 1, 3, 5, 7, 9, 11, 13 and 15, or a fragment thereof. The invention also includes a mutant or variant *AAP*, any of whose bases may be changed from the corresponding base shown in Tables 1, 3, 5, 7, 9, 11, 13 and 15 while still encoding a protein that maintains the activities and physiological functions of the AAP fragment, or a fragment of such a nucleic acid. The invention further includes nucleic acids whose sequences are complementary to those just described, including complementary nucleic acid fragments. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications. Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as anti-sense binding nucleic acids in therapeutic applications in a subject. In the mutant or variant nucleic acids, and their complements, up to 20% or more of the bases may be so changed.

The novel AAP of the invention include the protein fragments whose sequences are provided in Tables 2, 4, 6, 8, 10, 12, 14 and 16. The invention also includes an AAP mutant or variant protein, any of whose residues may be changed from the corresponding residue shown in Tables 2, 4, 6, 8, 10, 12, 14 and 16 while still encoding a protein that maintains its native activities and physiological functions, or a functional fragment thereof. In the mutant or variant AAP, up to 20% or more of the residues may be so changed. The invention further encompasses Abs and antibody fragments, such as F_{ab} or $(F_{ab})'_2$, that bind immunospecifically to any of the AAP of the invention.

The AAP nucleic acids are shown in Tables 1, 3, 5, 7, 9, 11, 13 and 15, and the corresponding polypeptides are shown in Tables 2, 4, 6, 8, 10, 12, 14 and 16, respectivly. Start and stop codons in the polynucleotide sequences are indicated in **boldface** and with underlining. SEQ ID NO:3 lacks a stop codon. The sequences of *hMX1* and *hMX2* do not have start codons (see Table 17); consequently, hMX1 and hMX2 polypeptides do not start with a Met. For any lacking polynucleotide sequence, one of skill in the art may

retrieve the full length sequence by, for example, probing cDNA or genomic libraries with probes designed according to the sequences of the instant invention.

Table 1 KLP nucleotide sequence (SEQ ID NO:1)

ctggcctaga tactacaact gaacttttt tctttttagt tactccacag gatccgctga	60
acataggatg ttgccacaaa atctacctcg tgtatttttc tctttcactc atgagctgca	120
caattgcaga tttgagcaca atgtctgcag actgtgttga aaaactctga agaacctaat	180
taacacagga tgacctagga gtgattctaa gtctgtgtaa caagatatta ctcattagtg	240
aatgtgtcag tcttggtact gaatgctgca gataacagca agtaggttct cctttatttc	300
tgaagtattc acttgacctt ccatcagtaa gacggacttt tctaatctgt tcctggagat	360
attaatggaa tacagtc**atg** tccactcaag acgagaggca gatcaatact gaatatgctg	420
tgtcattgtt ggaacagttg aaactgtttt atgaacagca gttgtttact gacatagtgt	480
taattgttga gggcactgaa ttcccttgtc ataagatggt tcttgcaaca tgtagctctt	540
atttcagggc catgtttatg agtggactaa gtgaaagcaa acaaacccat gtacacctga	600
ggaatgtcga tgctgccacc ttacagataa taataactta tgcatacacg ggtaacttgg	660
caatgaatga cagcactgta gaacagcttt atgaaacagc ttgcttccta caggtagaag	720
atgtgttaca acgttgtcga gaatatttaa ttaaaaaaat aaatgcagag aattgtgtac	780
gattgttgag ttttgctgat ctcttcagtt gtgaggaatt aaaacagagt gctaaaagaa	840
tggtggagca caagttcact gctgtgtatc atcaggacgc gttcatgcag ctgtcacatg	900
acctactgat agatattctc agtagtgaca atttaaatgt agaaaaggaa gaaaccgttc	960
gagaagctgc tatgctgtgg ctagagtata acacagaatc acgatcccag tatttgtctt	1020
ctgttcttag ccaaatcaga attgatgcac tttcagaagt aacacagaga gcttggtttc	1080
aaggtctgcc acccaatgat aagtcagtgg tggttcaagg tctgtataag tccatgccca	1140
agtttttcaa accaagactt gggatgacta aagaggaaat gatgattttc attgaagcat	1200
cttcagaaaa tccttgtagt ctttactctt ctgtctgtta cagcccccaa gcagaaaaag	1260
tttacaagtt atgtagccca ccagctgatt tgcataaggt tgggaccgtt gtaactcctg	1320
ataatgatat ctacatagca gggggtcaag ttcctctgaa aaacacaaaa acaaatcaca	1380
gtaaaacaag caaacttcag actgccttca gaactgtgaa ttgcttttat tggtttgatg	1440
cacagcaaaa tacctggttt ccaaagaccc caatgctttt tgtccgcata aagccatctt	1500
tggtttgctg tgaaggctat atctatgcaa ttggaggaga tagcgtaggt ggagaactta	1560
atcggaggac cgtagaaaga tacgacactg agaaagatga gtggacgatg gtaagccctt	1620
taccttgtgc ttggcaatgg agtgcagcag ttgtggttca tgactgcatt tatgtgatga	1680
cactgaacct catgtactgt tattttccaa ggtctgactc atgggtagaa atggccatga	1740
gacagactag taggtccttt gcttcagctg cagcttttgg tgataaaatt ttctatattg	1800
gagggttgca tattgctacc aattccggca taagactccc ctctggcact gtagatgggt	1860
cttcagtaac tgtggaaatt tatgatgtga ataaaaatga gtggaaaatg gcagccaaca	1920
tccctgctaa gaggtactct gacccctgtg ttagagctgt tgtgatctca aattctctat	1980
gtgtgtttat gcgagaaacc cacttaaatg agcgagctaa atacgtcacc taccaatatg	2040
acctggaact tgaccggtgg tctctgcggc agcatatatc tgaacgtgta ctgtgggact	2100
tggggagaga ttttcgatgc actgtgggga aactctatcc atcctgcctt gaagagtctc	2160
catggaaacc accaacttat ctttttcaa cggatgggac agaagagttt gaactggatg	2220
gagaaatggt tgcactacca cctgta**tag**t ggggaagttc agggagtgca cgcctgagtt	2280

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atgtgctttg tcattttctt tgctaaacaa aagaggctat gaaagaacta aatatgagta    2340
cataaaattc tatctttgat aaattttatt tttatgccct acttaatatt tgcatcagta    2400
taatatatat cagtgagtct tacagaaaga tatgcttcca taatatgaaa tagattattc    2460
aataattgag aaactttatg tgtaatcatg agagtataag aatctggatt atctaacatt    2520
gttagccctg tgtatgtaca gttcaaaaag ttcatttata aaagtagttt cctgttc       2577
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Table 2 KLP polypeptide sequence (SEQ ID NO:2)

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Met Ser Thr Gln Asp Glu Arg Gln Ile Asn Thr Glu Tyr Ala Val Ser
1               5                  10                  15

Leu Leu Glu Gln Leu Lys Leu Phe Tyr Glu Gln Gln Leu Phe Thr Asp
            20                  25                  30

Ile Val Leu Ile Val Glu Gly Thr Glu Phe Pro Cys His Lys Met Val
        35                  40                  45

Leu Ala Thr Cys Ser Ser Tyr Phe Arg Ala Met Phe Met Ser Gly Leu
    50                  55                  60

Ser Glu Ser Lys Gln Thr His Val His Leu Arg Asn Val Asp Ala Ala
65                  70                  75                  80

Thr Leu Gln Ile Ile Ile Thr Tyr Ala Tyr Thr Gly Asn Leu Ala Met
                85                  90                  95

Asn Asp Ser Thr Val Glu Gln Leu Tyr Glu Thr Ala Cys Phe Leu Gln
            100                 105                 110

Val Glu Asp Val Leu Gln Arg Cys Arg Glu Tyr Leu Ile Lys Lys Ile
        115                 120                 125

Asn Ala Glu Asn Cys Val Arg Leu Leu Ser Phe Ala Asp Leu Phe Ser
    130                 135                 140

Cys Glu Glu Leu Lys Gln Ser Ala Lys Arg Met Val Glu His Lys Phe
145                 150                 155                 160

Thr Ala Val Tyr His Gln Asp Ala Phe Met Gln Leu Ser His Asp Leu
                165                 170                 175

Leu Ile Asp Ile Leu Ser Ser Asp Asn Leu Asn Val Glu Lys Glu Glu
            180                 185                 190

Thr Val Arg Glu Ala Ala Met Leu Trp Leu Glu Tyr Asn Thr Glu Ser
        195                 200                 205

Arg Ser Gln Tyr Leu Ser Ser Val Leu Ser Gln Ile Arg Ile Asp Ala
    210                 215                 220

Leu Ser Glu Val Thr Gln Arg Ala Trp Phe Gln Gly Leu Pro Pro Asn
225                 230                 235                 240

Asp Lys Ser Val Val Val Gln Gly Leu Tyr Lys Ser Met Pro Lys Phe
                245                 250                 255

Phe Lys Pro Arg Leu Gly Met Thr Lys Glu Glu Met Met Ile Phe Ile
            260                 265                 270
```

Glu Ala Ser Ser Glu Asn Pro Cys Ser Leu Tyr Ser Ser Val Cys Tyr
275 280 285

Ser Pro Gln Ala Glu Lys Val Tyr Lys Leu Cys Ser Pro Pro Ala Asp
290 295 300

Leu His Lys Val Gly Thr Val Val Thr Pro Asp Asn Asp Ile Tyr Ile
305 310 315 320

Ala Gly Gly Gln Val Pro Leu Lys Asn Thr Lys Thr Asn His Ser Lys
325 330 335

Thr Ser Lys Leu Gln Thr Ala Phe Arg Thr Val Asn Cys Phe Tyr Trp
340 345 350

Phe Asp Ala Gln Gln Asn Thr Trp Phe Pro Lys Thr Pro Met Leu Phe
355 360 365

Val Arg Ile Lys Pro Ser Leu Val Cys Cys Glu Gly Tyr Ile Tyr Ala
370 375 380

Ile Gly Gly Asp Ser Val Gly Gly Glu Leu Asn Arg Arg Thr Val Glu
385 390 395 400

Arg Tyr Asp Thr Glu Lys Asp Glu Trp Thr Met Val Ser Pro Leu Pro
405 410 415

Cys Ala Trp Gln Trp Ser Ala Ala Val Val Val His Asp Cys Ile Tyr
420 425 430

Val Met Thr Leu Asn Leu Met Tyr Cys Tyr Phe Pro Arg Ser Asp Ser
435 440 445

Trp Val Glu Met Ala Met Arg Gln Thr Ser Arg Ser Phe Ala Ser Ala
450 455 460

Ala Ala Phe Gly Asp Lys Ile Phe Tyr Ile Gly Gly Leu His Ile Ala
465 470 475 480

Thr Asn Ser Gly Ile Arg Leu Pro Ser Gly Thr Val Asp Gly Ser Ser
485 490 495

Val Thr Val Glu Ile Tyr Asp Val Asn Lys Asn Glu Trp Lys Met Ala
500 505 510

Ala Asn Ile Pro Ala Lys Arg Tyr Ser Asp Pro Cys Val Arg Ala Val
515 520 525

Val Ile Ser Asn Ser Leu Cys Val Phe Met Arg Glu Thr His Leu Asn
530 535 540

Glu Arg Ala Lys Tyr Val Thr Tyr Gln Tyr Asp Leu Glu Leu Asp Arg
545 550 555 560

Trp Ser Leu Arg Gln His Ile Ser Glu Arg Val Leu Trp Asp Leu Gly
565 570 575

Arg Asp Phe Arg Cys Thr Val Gly Lys Leu Tyr Pro Ser Cys Leu Glu
580 585 590

Glu Ser Pro Trp Lys Pro Pro Thr Tyr Leu Phe Ser Thr Asp Gly Thr
595 600 605

Glu Glu Phe Glu Leu Asp Gly Glu Met Val Ala Leu Pro Pro Val
610 615 620

Table 3 hBAZF nucleotide sequence (SEQ ID NO:3)

```
caagggagcg agggtgtcgt agagggcaga atgaacaaga agaattagga gggaggctgc      60
gtgtgccggg gctaggggct ggaagtcctg gctctagttg cacctcggaa ggaaaaggca     120
aacagaggag ggaaggcgtc ttaggactgc ctggatccag agcactttcc tcggcctcta     180
caggcctgtg tcgctatggg ttcccccgcc gccccggagg gagcgctggg ctacgtccgc     240
gagttcactc gccactcctc cgacgtgctg ggcaacctca acgagctgcg cctgcgcggg     300
atcctcactg acgtcacgct gctggttggc gggcaacccc tcagagcaca caaggcagtt     360
ctcatcgcct gcagtggctt cttctattca attttccggg gccgtgcggg agtcggggtg     420
gacgtgctct ctctgcccgg gggtcccgaa gcgagaggct tcgcccctct attggacttc     480
atgtacactt cgcgcctgcg cctctctcca gccactgcac cagcagtcct agcggccgcc     540
acctatttgc agatggagca cgtggtccag gcatgccacc gcttcatcca ggccagctat     600
gaacctctgg gcatctccct gcgccccctg gaagcagaac ccccaacacc cccaacggcc     660
cctccaccag gtagtcccag gcgctccgaa ggacacccag acccacctac tgaatctcga     720
agctgcagtc aaggcccccc cagtccagcc agccctgacc ccaaggcctg caactggaaa     780
aagtacaagt acatcgtgct aaactctcag gcctcccaag cagggagcct ggtcggggag     840
agaagttctg gtccaaccttg cccccaagcc aggctcccca gtggagacga ggcctccagc     900
agcagcagca gcagcagcag cagcagcagt gaagaaggac ccattcctgg tccccagagc     960
aggctctctc caactgctgc cactgtgcag ttcaaatgtg gggctccagc cagtaccccc    1020
tacctcctca catcccaggc tcaagacacc tctggatcac cctctgaacg ggctcgtcca    1080
ctacccggga gtgaattttt cagctgccag aactgtgagg ctgtggcagg gtgctcatcg    1140
gggctggact ccttggttcc tggggacgaa gacaaaccct ataagtgtca gctgtgccgg    1200
tcttcgttcc gctacaaggg caaccttgcc agtcaccgta cagtgcacac aggggaaaag    1260
ccttaccact gctcaatctg cggagcccgt tttaaccggc cagcaaacct gaaaacgcac    1320
agccgcatcc attcgggaga gaagccgtat aagtgtgaga cgtgcggctc gcgctttgta    1380
caggtacgga gccagcctcc aagtggcttc caaggcaaac ctgcaagagg tggggtgggc    1440
caaaagggag ggttctgttc ctcccagagg caggacttga agtctcctcc ctcccaggtg    1500
gcacatctgc gggcgcacgt gctgatccac accggggaga agccctaccc ttgccctacc    1560
tgcggaaccc gcttccgcca cctgcagacc ctcaagagcc acgttcgcat ccacaccgga    1620
gagaagcctt accactgcga cccctgtggc ctgcatttcc ggcacaagag tcaactgcgg    1680
ctgcatctgc gccagaaaca cggagctgct accaacacca aagtgcacta ccacattctc    1740
ggggggccc                                                            1749
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Table 4 hBAZF polypeptide sequence (SEQ ID NO:4)

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Met Gly Ser Pro Ala Ala Pro Glu Gly Ala Leu Gly Tyr Val Arg Glu
1               5                  10                  15

Phe Thr Arg His Ser Ser Asp Val Leu Gly Asn Leu Asn Glu Leu Arg
            20                  25                  30

Leu Arg Gly Ile Leu Thr Asp Val Thr Leu Leu Val Gly Gly Gln Pro
        35                  40                  45
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Leu Arg Ala His Lys Ala Val Leu Ile Ala Cys Ser Gly Phe Phe Tyr
    50                  55                  60

Ser Ile Phe Arg Gly Arg Ala Gly Val Gly Val Asp Val Leu Ser Leu
65                  70                  75                  80

Pro Gly Gly Pro Glu Ala Arg Gly Phe Ala Pro Leu Leu Asp Phe Met
                85                  90                  95

Tyr Thr Ser Arg Leu Arg Leu Ser Pro Ala Thr Ala Pro Ala Val Leu
            100                 105                 110

Ala Ala Ala Thr Tyr Leu Gln Met Glu His Val Val Gln Ala Cys His
        115                 120                 125

Arg Phe Ile Gln Ala Ser Tyr Glu Pro Leu Gly Ile Ser Leu Arg Pro
    130                 135                 140

Leu Glu Ala Glu Pro Pro Thr Pro Pro Thr Ala Pro Pro Pro Gly Ser
145                 150                 155                 160

Pro Arg Arg Ser Glu Gly His Pro Asp Pro Pro Thr Glu Ser Arg Ser
                165                 170                 175

Cys Ser Gln Gly Pro Pro Ser Pro Ala Ser Pro Asp Pro Lys Ala Cys
            180                 185                 190

Asn Trp Lys Lys Tyr Lys Tyr Ile Val Leu Asn Ser Gln Ala Ser Gln
        195                 200                 205

Ala Gly Ser Leu Val Gly Glu Arg Ser Ser Gly Gln Pro Cys Pro Gln
    210                 215                 220

Ala Arg Leu Pro Ser Gly Asp Glu Ala Ser Ser Ser Ser Ser Ser Ser
225                 230                 235                 240

Ser Ser Ser Ser Ser Glu Glu Gly Pro Ile Pro Gly Pro Gln Ser Arg
                245                 250                 255

Leu Ser Pro Thr Ala Ala Thr Val Gln Phe Lys Cys Gly Ala Pro Ala
            260                 265                 270

Ser Thr Pro Tyr Leu Leu Thr Ser Gln Ala Gln Asp Thr Ser Gly Ser
        275                 280                 285

Pro Ser Glu Arg Ala Arg Pro Leu Pro Gly Ser Glu Phe Phe Ser Cys
    290                 295                 300

Gln Asn Cys Glu Ala Val Ala Gly Cys Ser Ser Gly Leu Asp Ser Leu
305                 310                 315                 320

Val Pro Gly Asp Glu Asp Lys Pro Tyr Lys Cys Gln Leu Cys Arg Ser
                325                 330                 335

Ser Phe Arg Tyr Lys Gly Asn Leu Ala Ser His Arg Thr Val His Thr
            340                 345                 350

Gly Glu Lys Pro Tyr His Cys Ser Ile Cys Gly Ala Arg Phe Asn Arg
        355                 360                 365

Pro Ala Asn Leu Lys Thr His Ser Arg Ile His Ser Gly Glu Lys Pro
    370                 375                 380

Tyr Lys Cys Glu Thr Cys Gly Ser Arg Phe Val Gln Val Arg Ser Gln
385                 390                 395                 400
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Pro Pro Ser Gly Phe Gln Gly Lys Pro Ala Arg Gly Gly Val Gly Gln
               405                 410                 415

Lys Gly Gly Phe Cys Ser Ser Gln Arg Gln Asp Leu Lys Ser Pro Pro
           420                 425                 430

Ser Gln Val Ala His Leu Arg Ala His Val Leu Ile His Thr Gly Glu
       435                 440                 445

Lys Pro Tyr Pro Cys Pro Thr Cys Gly Thr Arg Phe Arg His Leu Gln
   450                 455                 460

Thr Leu Lys Ser His Val Arg Ile His Thr Gly Glu Lys Pro Tyr His
465                 470                 475                 480

Cys Asp Pro Cys Gly Leu His Phe Arg His Lys Ser Gln Leu Arg Leu
               485                 490                 495

His Leu Arg Gln Lys His Gly Ala Ala Thr Asn Thr Lys Val His Tyr
           500                 505                 510

His Ile Leu Gly Gly Pro
       515
```

Table 5 hEF-G nucleotide sequence (SEQ ID NO:5)

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cgcgtgctct gcgcttgcc**a** **tg**agactcct gggagctgca gccgtcgcgg ctctggggcg	180
cggaagggcc cccgcctccc taggctggca gaggaagcag gttaattgga aggcctgccg	240
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cattgattct gggaaaacta cattaacaga acgagtcctt tactacactg gcagaattgc	360
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caatattaac attatagata ctcctgggca tgtggacttc acaatagaag tggaaagggc	540
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gaccatgact gtcaatcgtc agatgaagcg ctacaacgtt ccgtttctaa cttttattaa	660
caaattggac cgaatgggct ccaacccagc cagggccctg cagcaaatga ggtctaaact	720
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agaatacctc ccaaatccat ctgaagtcca gaactatgct attctcaata aaaaggatga	1140
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gttgcaacgg ctggctcgca tgcatgccga catgatggag gcaagtacag aggaagtata	1380
tgccggagac atctgtgcat tgtttggcat tgactgtgct agtggagaca cattcacaga	1440

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caaagccaac agcggccttt ctatggagtc aattcatgtt cctgatcctg tcatttcaat   1500
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tacaagagaa gatcccacat ttaaagtata ctttgacact gagaacaaag agacagttat   1620
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tcttaaacaa gccttggcaa atgcaacatt atgtattctt gaacctatta tggctgtgga   2100
agttgtagct ccaaatgaat ttcagggaca agtaattgca ggaattaacc gacgccatgg   2160
ggtaatcact gggcaagatg gagttgagga ctattttaca ctgtatgcag atgtccctct   2220
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cacaatggag tatagcaggt atcagccatg tttaccatcc acacaagaag acgtcattaa   2340
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aatcaaatgt aatttataga gttagtttca tcaacctaat gaatgctagt taaatttgaa   3300
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tttgtttcca gaaaaagttg ggctttccca agcagttcta ttacccggtt cagaattgct   3420
tcatccaaaa atcatctgat ggtatagatg gatcctagtc cttttcatta cctgatggta   3480
gaaataaaat aattgatttt a                                             3501
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Table 6 hEF-G polypeptide (SEQ ID NO:6)

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Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
1               5                  10                  15

Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
            20                  25                  30

Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
        35                  40                  45
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Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys Thr Thr Leu Thr Glu
    50                  55                  60

Arg Val Leu Tyr Tyr Thr Gly Arg Ile Ala Lys Met His Glu Val Lys
65                  70                  75                  80

Gly Lys Asp Gly Val Gly Ala Val Met Asp Ser Met Glu Leu Glu Arg
                85                  90                  95

Gln Arg Gly Ile Thr Ile Gln Ser Ala Ala Thr Phe Thr Met Trp Lys
            100                 105                 110

Asp Val Asn Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr
        115                 120                 125

Ile Glu Val Glu Arg Ala Leu Arg Val Leu Asp Gly Ala Val Leu Val
    130                 135                 140

Leu Cys Ala Val Gly Gly Val Gln Cys Gln Thr Met Thr Val Asn Arg
145                 150                 155                 160

Gln Met Lys Arg Tyr Asn Val Pro Phe Leu Thr Phe Ile Asn Lys Leu
                165                 170                 175

Asp Arg Met Gly Ser Asn Pro Ala Arg Ala Leu Gln Gln Met Arg Ser
            180                 185                 190

Lys Leu Asn His Asn Thr Ala Phe Met Gln Ile Pro Met Gly Leu Glu
        195                 200                 205

Gly Asn Phe Lys Gly Ile Val Asp Leu Ile Glu Glu Arg Ala Ile Tyr
    210                 215                 220

Phe Asp Gly Asp Phe Ser Gln Ile Val Arg Tyr Gly Glu Ile Pro Ala
225                 230                 235                 240

Glu Leu Arg Ala Ala Ala Thr Asp His Arg Gln Glu Leu Ile Glu Cys
                245                 250                 255

Val Ala Asn Ser Asp Glu Gln Leu Gly Glu Met Phe Leu Glu Glu Lys
            260                 265                 270

Ile Pro Ser Ile Ser Asp Leu Lys Leu Ala Ile Arg Arg Ala Thr Leu
        275                 280                 285

Lys Arg Ser Phe Thr Pro Val Phe Leu Gly Ser Ala Leu Lys Asn Lys
    290                 295                 300

Gly Val Gln Pro Leu Leu Asp Ala Val Leu Glu Tyr Leu Pro Asn Pro
305                 310                 315                 320

Ser Glu Val Gln Asn Tyr Ala Ile Leu Asn Lys Lys Asp Asp Ser Lys
                325                 330                 335

Glu Lys Thr Lys Ile Leu Met Asn Ser Ser Arg His Asn Ser His Pro
            340                 345                 350

Phe Val Gly Leu Ala Phe Pro Leu Glu Val Gly Arg Phe Gly Gln Leu
        355                 360                 365

Thr Tyr Val Arg Ser Tyr Gln Gly Glu Leu Lys Lys Gly Asp Thr Ile
    370                 375                 380

Tyr Asn Thr Arg Thr Arg Lys Lys Val Arg Leu Gln Arg Leu Ala Arg
385                 390                 395                 400
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Met His Ala Asp Met Met Glu Ala Ser Thr Glu Glu Val Tyr Ala Gly
405 410 415

Asp Ile Cys Ala Leu Phe Gly Ile Asp Cys Ala Ser Gly Asp Thr Phe
420 425 430

Thr Asp Lys Ala Asn Ser Gly Leu Ser Met Glu Ser Ile His Val Pro
435 440 445

Asp Pro Val Ile Ser Ile Ala Met Lys Pro Ser Asn Lys Asn Asp Leu
450 455 460

Glu Lys Phe Ser Lys Gly Ile Gly Arg Phe Thr Arg Glu Asp Pro Thr
465 470 475 480

Phe Lys Val Tyr Phe Asp Thr Glu Asn Lys Glu Thr Val Ile Ser Gly
485 490 495

Met Gly Glu Leu His Leu Glu Ile Tyr Ala Gln Arg Leu Glu Arg Glu
500 505 510

Tyr Gly Cys Pro Cys Ile Thr Gly Lys Pro Lys Val Ala Phe Arg Glu
515 520 525

Thr Ile Thr Ala Pro Val Pro Phe Asp Phe Thr His Lys Lys Gln Ser
530 535 540

Gly Gly Ala Gly Gln Tyr Gly Lys Val Ile Gly Val Leu Glu Pro Leu
545 550 555 560

Asp Pro Glu Asp Tyr Thr Lys Leu Glu Phe Ser Asp Glu Thr Phe Gly
565 570 575

Ser Asn Ile Pro Lys Gln Phe Val Pro Ala Val Glu Lys Gly Phe Leu
580 585 590

Asp Ala Cys Glu Lys Gly Pro Leu Ser Gly His Lys Leu Ser Gly Leu
595 600 605

Arg Phe Val Leu Gln Asp Gly Ala His His Met Val Asp Ser Asn Glu
610 615 620

Ile Ser Phe Ile Arg Ala Gly Glu Gly Ala Leu Lys Gln Ala Leu Ala
625 630 635 640

Asn Ala Thr Leu Cys Ile Leu Glu Pro Ile Met Ala Val Glu Val Val
645 650 655

Ala Pro Asn Glu Phe Gln Gly Gln Val Ile Ala Gly Ile Asn Arg Arg
660 665 670

His Gly Val Ile Thr Gly Gln Asp Gly Val Glu Asp Tyr Phe Thr Leu
675 680 685

Tyr Ala Asp Val Pro Leu Asn Asp Met Phe Gly Tyr Ser Thr Glu Leu
690 695 700

Arg Ser Cys Thr Glu Gly Lys Gly Glu Tyr Thr Met Glu Tyr Ser Arg
705 710 715 720

Tyr Gln Pro Cys Leu Pro Ser Thr Gln Glu Asp Val Ile Asn Lys Tyr
725 730 735

Leu Glu Ala Thr Gly Gln Leu Pro Val Lys Lys Gly Lys Ala Lys Asn
740 745 750

Table 7 hTRG nucleotide sequence (SEQ ID NO:7)

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gccgagctgc ggcagagcgt gtctgaggtg gtgcgcggct ccgtgctcct ggcaaagcca	180
aagctaattg agccactcga ctatgaaaat gtcatcgtcc agaagaagac tcagatcctg	240
aacgactgtt tacgggagat gctgctcttc ccttacgatg actttcagac ggccatcctg	300
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ctgtacatat atgtattaca tttctacatt tttaatactc acatgggctt atgcattaag	7140
tttaattgtg ataaatttgt gctgttccag tatatgcaat acactttaat gttttattct	7200
tgtacataaa aatgtgcaat atggagatgt atacagtctt tactatatta ggtttataaa	7260
cagttttaag aatttcatcc ttttgccaaa atggtggagt atgtaattgg taaatcataa	7320
atcctgtggt gaatggtggt gtactttaaa gctgtcacca tgttatattt tcttttaaga	7380
ctttaattta gtaattttat atttgggaaa ataaaggttt ttaattttat ttaactggaa	7440
tcactgccct gctgtaatta aacattctgt accacatctg tattaaaaag acattgctga	7500
ccatta	7506

Table 8 hTRG polypeptide sequence (SEQ ID NO:8)

```
Met Ser Gln Pro Pro Leu Leu Pro Ala Ser Ala Glu Thr Arg Lys Phe
1               5                  10                  15

Thr Arg Ala Leu Ser Lys Pro Gly Thr Ala Ala Glu Leu Arg Gln Ser
            20                  25                  30

Val Ser Glu Val Val Arg Gly Ser Val Leu Leu Ala Lys Pro Lys Leu
        35                  40                  45

Ile Glu Pro Leu Asp Tyr Glu Asn Val Ile Val Gln Lys Lys Thr Gln
    50                  55                  60

Ile Leu Asn Asp Cys Leu Arg Glu Met Leu Leu Phe Pro Tyr Asp Asp
65                  70                  75                  80

Phe Gln Thr Ala Ile Leu Arg Arg Gln Gly Arg Tyr Ile Cys Ser Thr
                85                  90                  95

Val Pro Ala Lys Ala Glu Glu Glu Ala Gln Ser Leu Phe Val Thr Glu
            100                 105                 110

Cys Ile Lys Thr Tyr Asn Ser Asp Trp His Leu Val Asn Tyr Lys Tyr
        115                 120                 125

Glu Asp Tyr Ser Gly Glu Phe Arg Gln Leu Pro Asn Lys Val Val Lys
    130                 135                 140

Leu Asp Lys Leu Pro Val His Val Tyr Glu Val Asp Glu Glu Val Asp
145                 150                 155                 160

Lys Asp Glu Asp Ala Ala Ser Leu Gly Ser Gln Lys Gly Gly Ile Thr
                165                 170                 175

Lys His Gly Trp Leu Tyr Lys Gly Asn Met Asn Ser Ala Ile Ser Val
            180                 185                 190

Thr Met Arg Ser Phe Lys Arg Arg Phe Phe His Leu Ile Gln Leu Gly
        195                 200                 205

Asp Gly Ser Tyr Lys Phe Glu Phe Leu Lys Asp Leu Gln Lys Glu Pro
    210                 215                 220

Lys Gly Ser Ile Phe Leu Gly Phe Leu Tyr Gly Val Ser Phe Arg Asn
225                 230                 235                 240

Asn Lys Val Arg Arg Phe Ala Phe Glu Leu Lys Met Gln Asp Lys Ser
                245                 250                 255

Ser Tyr Leu Leu Ala Ala Asp Ser Glu Val Glu Met Glu Glu Trp Ile
            260                 265                 270

Thr Ile Leu Asn Lys Ile Leu Gln Leu Asn Phe Glu Ala Ala Met Gln
        275                 280                 285

Glu Lys Arg Asn Gly Asp Ser His Glu Asp Asp Glu Gln Ser Lys Leu
    290                 295                 300

Glu Gly Ser Gly Ser Gly Leu Asp Ser Tyr Leu Pro Glu Leu Ala Lys
305                 310                 315                 320

Ser Ala Arg Glu Ala Glu Ile Lys Leu Lys Ser Glu Ser Arg Val Lys
                325                 330                 335

Leu Phe Tyr Leu Asp Pro Asp Ala Gln Lys Leu Asp Phe Ser Ser Ala
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            340                 345                 350

Glu Pro Glu Val Lys Ser Phe Glu Glu Lys Phe Gly Lys Arg Ile Leu
        355                 360                 365

Val Lys Cys Asn Asp Leu Ser Phe Asn Leu Gln Cys Cys Val Ala Glu
    370                 375                 380

Asn Glu Glu Gly Pro Thr Thr Asn Val Glu Pro Phe Phe Val Thr Leu
385                 390                 395                 400

Ser Leu Phe Asp Ile Lys Tyr Asn Arg Lys Ile Ser Ala Asp Phe His
                405                 410                 415

Val Asp Leu Asn His Phe Ser Val Arg Gln Met Ile Ala Thr Thr Ser
            420                 425                 430

Pro Ala Leu Met Asn Gly Ser Gly Pro Glu Thr Gln Ser Ala Leu Arg
        435                 440                 445

Gly Ile Leu His Glu Ala Ala Met Gln Tyr Pro Lys Gln Gly Ile Phe
    450                 455                 460

Ser Val Thr Cys Pro His Pro Asp Ile Phe Leu Val Ala Arg Ile Glu
465                 470                 475                 480

Lys Val Leu Gln Gly Ser Ile Thr His Cys Ala Glu Pro Tyr Met Lys
                485                 490                 495

Ser Ser Asp Ser Ser Lys Val Ala Gln Lys Val Leu Lys Asn Ala Lys
            500                 505                 510

Gln Ala Cys Gln Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp Ala
        515                 520                 525

Ala Arg Thr Leu Phe Lys Asp Ala Ser Gly Asn Leu Asp Lys Asn Ala
    530                 535                 540

Arg Phe Ser Ala Ile Tyr Arg Gln Asp Ser Asn Lys Leu Ser Asn Asp
545                 550                 555                 560

Asp Met Leu Lys Leu Leu Ala Asp Phe Arg Lys Pro Glu Lys Met Ala
                565                 570                 575

Lys Leu Pro Val Ile Leu Gly Asn Leu Asp Ile Thr Ile Asp Asn Val
            580                 585                 590

Ser Ser Asp Phe Pro Asn Tyr Val Asn Ser Ser Tyr Ile Pro Thr Lys
        595                 600                 605

Gln Phe Glu Thr Cys Ser Lys Thr Pro Ile Thr Phe Glu Val Glu Glu
    610                 615                 620

Phe Val Pro Cys Ile Pro Lys His Thr Gln Pro Tyr Thr Ile Tyr Thr
625                 630                 635                 640

Asn His Leu Tyr Val Tyr Pro Lys Tyr Leu Lys Tyr Asp Ser Gln Lys
                645                 650                 655

Ser Phe Ala Lys Ala Arg Asn Ile Ala Ile Cys Ile Glu Phe Lys Asp
            660                 665                 670

Ser Asp Glu Glu Asp Ser Gln Pro Leu Lys Cys Ile Tyr Gly Arg Pro
        675                 680                 685

Gly Gly Pro Val Phe Thr Arg Ser Ala Phe Ala Ala Val Leu His His
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     690                 695                 700

His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile Glu Leu Pro Thr
705                 710                 715                 720

Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe Phe His Val Ser
                725                 730                 735

Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg Asp Val Val Glu
            740                 745                 750

Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys Asp Gly Arg Val
        755                 760                 765

Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn Leu Pro Ser Gly
    770                 775                 780

Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His Tyr Gly Pro Glu
785                 790                 795                 800

Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys Ile Ser Thr His
                805                 810                 815

Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu His Asn Phe Phe
            820                 825                 830

Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala Leu Gly Asn Glu
        835                 840                 845

Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu Gly His Val Met
    850                 855                 860

Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg Val Leu Thr
865                 870                 875                 880

Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr Arg Val Ile Ile
                885                 890                 895

His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu Ser His Leu Arg
            900                 905                 910

Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val Ala Ser Glu
        915                 920                 925

Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met Thr Thr Ile Leu
    930                 935                 940

Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu Lys Tyr Ser
945                 950                 955                 960

Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala Gln His Leu Ile
                965                 970                 975

Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg Phe Pro Ala Ser
            980                 985                 990

Tyr His His Ala Val Glu Thr Val  Val Asn Met Leu Met  Pro His
Ile
        995                 1000                1005

Thr Gln  Lys Phe Arg Asp Asn  Pro Glu Ala Ser Lys  Asn Ala Asn
    1010                1015                1020

His Ser  Leu Ala Val Phe Ile  Lys Arg Cys Phe Thr  Phe Met Asp
    1025                1030                1035
```

Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe
1040 1045 1050

Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe
1055 1060 1065

Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu
1070 1075 1080

Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu
1085 1090 1095

Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
1100 1105 1110

Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu
1115 1120 1125

Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
1130 1135 1140

Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His
1145 1150 1155

Gln Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu
1160 1165 1170

Ile Glu Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe
1175 1180 1185

Pro Val Asn Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu
1190 1195 1200

Pro Ala Val Asn Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu
1205 1210 1215

Asp Asn Ser Leu His Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile
1220 1225 1230

Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn Ser Val Arg
1235 1240 1245

Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn
1250 1255 1260

Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys
1265 1270 1275

His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp
1280 1285 1290

Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu
1295 1300 1305

Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp
1310 1315 1320

Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser
1325 1330 1335

Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
1340 1345 1350

Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly Ser
1355 1360 1365

Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	Ser	Asp
	1370					1375					1380			
Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	Thr
	1385					1390					1395			
Glu	Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu
	1400					1405					1410			
Ala	Phe	Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu
	1415					1420					1425			
Met	Lys	Lys	Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His
	1430					1435					1440			
Gln	Ser	Glu	Thr	Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser
	1445					1450					1455			
Leu	Ile	Tyr	Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp
	1460					1465					1470			
Met	Cys	Ala	Ala	Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser
	1475					1480					1485			
Lys	Leu	Ser	Ser	Ile	Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe
	1490					1495					1500			
Leu	Met	Arg	Asn	Asn	Phe	Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val
	1505					1510					1515			
Arg	Thr	His	Leu	Gln	Val	Ile	Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala
	1520					1525					1530			
Asp	Val	Val	Gly	Ile	Gly	Gly	Thr	Arg	Phe	Gln	Gln	Ser	Leu	Ser
	1535					1540					1545			
Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp	Arg	Leu	Ile	Lys	His	Thr
	1550					1555					1560			
Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr
	1565					1570					1575			
Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Asn	Asp	Pro
	1580					1585					1590			
Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	Ala
	1595					1600					1605			
Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Arg
	1610					1615					1620			
Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr
	1625					1630					1635			
Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Glu
	1640					1645					1650			
Ala	Val	Gln	Trp	Glu	Pro	Pro	Leu	Leu	Pro	His	Ser	His	Ser	Ala
	1655					1660					1665			
Cys	Leu	Arg	Arg	Ser	Arg	Gly	Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr
	1670					1675					1680			
Ala	Phe	Arg	Val	Ile	Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met
	1685					1690					1695			

Met Glu Asp Val Gly Met Gln Asp Val His Phe Asn Glu Asp Val
1700 1705 1710

Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu Trp Lys Ala
1715 1720 1725

Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro
1730 1735 1740

Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu Tyr
1745 1750 1755

Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
1760 1765 1770

Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe
1775 1780 1785

Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser Glu Thr Asp Val
1790 1795 1800

Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys
1805 1810 1815

Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu
1820 1825 1830

Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile
1835 1840 1845

Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
1850 1855 1860

Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys
1865 1870 1875

Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile
1880 1885 1890

Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg
1895 1900 1905

Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
1910 1915 1920

Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met
1925 1930 1935

Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp
1940 1945 1950

Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser
1955 1960 1965

Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
1970 1975 1980

Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala
1985 1990 1995

Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val
2000 2005 2010

Lys Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly
2015 2020 2025

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Gln Ala  Leu Ala Val Asn Glu  Arg Leu Ile Lys Glu  Asp Gln Leu
    2030                 2035                 2040

Glu Tyr  Gln Glu Glu Met Lys  Ala Asn Tyr Arg Glu  Met Ala Lys
    2045                 2050                 2055

Glu Leu  Ser Glu Ile Met His  Glu Gln Ile Cys Pro  Leu Glu Glu
    2060                 2065                 2070

Lys Thr  Ser Val Leu Pro Asn  Ser Leu His Ile Phe  Asn Ala Ile
    2075                 2080                 2085

Ser Gly  Thr Pro Thr Ser Thr  Met Val His Gly Met  Thr Ser Ser
    2090                 2095                 2100

Ser Ser  Val Val
    2105
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Table 9 hMX1 nucleotide sequence (SEQ ID NO:9)

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cgagagtttg tgccttcccg agatgaaata gaagctctga tccacaggca ggaaatgaca   5100
tccacggtct attgccatgg cggcggctcc tgcaagatca ccatcaactc ccacaccacc   5160
gctggggagg tggtggagaa gctgatccga ggcctggcca tggaggacag caggaacatg   5220
tttgctttgt ttgaatacaa cggccacgtc gacaaagcca ttgaaagtcg aaccgtcgta   5280
gctgatgtct tagccaagtt tgaaaagctg gctgccacat ccgaggttgg ggacctgcca   5340
tggaaattct acttcaaact ttactgcttc ctggacacag acaacgtgcc aaaagacagt   5400
gtggagtttg catttatgtt tgaacaggcc cacgaagcgg ttatccatgg ccaccatcca   5460
gccccggaag aaaacctcca ggttcttgct gccctgcgac tccagtatct gcagggggat   5520
tatactctgc acgctgccat cccacctctc gaagaggttt attccctgca gagactcaag   5580
gcccgcatca gccagtcaac caaaaccttc acccttgtg aacggctgga gaagaggcgg   5640
acgagcttcc tagaggggac cctgaggcgg agcttccgga caggatccgt ggtccggcag   5700
aaggtcgagg aggagcagat gctggacatg tggattaagg aagaagtctc ctctgctcga   5760
gccagtatca ttgacaagtg gaggaaattt cagggaatga accaggaaca ggccatggcc   5820
aagtacatgg ccttgatcaa ggagtggcct ggctatggct cgacgctgtt tgatgtggag   5880
tgcaaggaag gtggcttccc tcaggaactc tggttgggtg tcagcgcgga cgccgtctcc   5940
gtctacaagc gtggagaggg aagaccactg gaagtcttcc agtatgaaca catcctctct   6000
tttggggcac ccctggcgaa tacgtataag atcgtggtcg atgagaggga gctgctcttt   6060
gaaaccagtg aggtagtgga tgtggccaag ctcatgaaag cctacatcag catgatcgtg   6120
aagaagcgct acagcacgac acgctccgcc agcagccagg gcagctccag g            6171
```

Table 10 hMX1 polypeptide sequence (SEQ ID NO:10)

```
Phe Cys Leu Gln Gly Thr Arg Val Trp Leu Arg Glu Asn Gly Gln His
1               5                  10                  15

Phe Pro Ser Thr Val Asn Ser Cys Ala Glu Gly Ile Val Val Phe Arg
            20                  25                  30

Thr Asp Tyr Gly Gln Val Phe Thr Tyr Lys Gln Ser Thr Ile Thr His
        35                  40                  45

Gln Lys Val Thr Ala Met His Pro Thr Asn Glu Glu Gly Val Asp Asp
```

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     50                  55                  60

Met Ala Ser Leu Thr Glu Leu His Gly Gly Ser Ile Met Tyr Asn Leu
65                  70                  75                  80

Phe Gln Arg Tyr Lys Arg Asn Gln Ile Trp Thr Tyr Ile Gly Ser Ile
                85                  90                  95

Leu Ala Ser Val Asn Pro Tyr Gln Pro Ile Ala Gly Leu Tyr Glu Pro
            100                 105                 110

Ala Thr Met Glu Gln Tyr Ser Arg Arg His Leu Gly Glu Leu Pro Pro
        115                 120                 125

His Ile Phe Ala Ile Ala Asn Glu Cys Tyr Arg Cys Leu Trp Lys Arg
    130                 135                 140

His Asp Asn Gln Cys Ile Leu Ile Lys Gly Glu Ser Gly Ala Gly Lys
145                 150                 155                 160

Thr Glu Ser Thr Lys Leu Ile Leu Lys Phe Leu Ser Val Ile Ser Gln
                165                 170                 175

Gln Ser Leu Glu Leu Ser Leu Lys Glu Lys Thr Ser Cys Val Glu Arg
            180                 185                 190

Ala Ile Leu Glu Ser Ser Pro Ile Met Glu Ala Phe Gly Asn Ala Lys
        195                 200                 205

Thr Val Tyr Asn Asn Asn Ser Ser Arg Phe Gly Lys Phe Val Gln Leu
    210                 215                 220

Asn Ile Cys Gln Lys Gly Asn Ile Gln Gly Gly Arg Ile Val Asp Cys
225                 230                 235                 240

Ile Leu Ser Ser Gln Asn Arg Val Val Arg Gln Asn Pro Gly Glu Arg
                245                 250                 255

Asn Tyr His Ile Phe Tyr Ala Leu Leu Ala Gly Leu Glu His Glu Glu
            260                 265                 270

Arg Glu Glu Phe Tyr Leu Ser Thr Pro Glu Asn Tyr His Tyr Leu Asn
        275                 280                 285

Gln Ser Gly Cys Val Glu Asp Lys Thr Ile Ser Asp Gln Glu Ser Phe
    290                 295                 300

Arg Glu Val Ile Thr Ala Met Asp Val Met Gln Phe Ser Lys Glu Glu
305                 310                 315                 320

Val Arg Glu Val Ser Arg Leu Leu Ala Gly Ile Leu His Leu Gly Asn
                325                 330                 335

Ile Glu Phe Ile Thr Ala Gly Gly Ala Gln Val Ser Phe Lys Thr Ala
            340                 345                 350

Leu Gly Arg Ser Ala Glu Leu Leu Gly Leu Asp Pro Thr Gln Leu Thr
        355                 360                 365

Asp Ala Leu Thr Gln Arg Ser Met Phe Leu Arg Gly Glu Glu Ile Leu
    370                 375                 380

Thr Pro Leu Asn Val Gln Gln Ala Val Asp Ser Arg Asp Ser Leu Ala
385                 390                 395                 400

Met Ala Leu Tyr Ala Cys Cys Phe Glu Trp Val Ile Lys Lys Ile Asn
```

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                405                 410                 415
Ser Arg Ile Lys Gly Asn Glu Asp Phe Lys Ser Ile Gly Ile Leu Asp
            420                 425                 430
Ile Phe Gly Phe Glu Asn Phe Glu Val Asn His Phe Glu Gln Phe Asn
        435                 440                 445
Ile Asn Tyr Ala Asn Glu Lys Leu Gln Glu Tyr Phe Asn Lys His Ile
    450                 455                 460
Phe Ser Leu Glu Gln Leu Glu Tyr Ser Arg Glu Gly Leu Val Trp Glu
465                 470                 475                 480
Asp Ile Asp Trp Ile Asp Asn Gly Glu Cys Leu Asp Leu Ile Glu Lys
                485                 490                 495
Lys Leu Gly Leu Leu Ala Leu Ile Asn Glu Glu Ser His Phe Pro Gln
            500                 505                 510
Ala Thr Asp Ser Thr Leu Leu Glu Lys Leu His Ser Gln His Ala Asn
        515                 520                 525
Asn His Phe Tyr Val Lys Pro Arg Val Ala Val Asn Asn Phe Gly Val
    530                 535                 540
Lys His Tyr Ala Gly Glu Val Gln Tyr Asp Val Arg Gly Ile Leu Glu
545                 550                 555                 560
Lys Asn Arg Asp Thr Phe Arg Asp Asp Leu Leu Asn Leu Leu Arg Glu
                565                 570                 575
Ser Arg Phe Asp Phe Ile Tyr Asp Leu Phe Glu His Val Ser Ser Arg
            580                 585                 590
Asn Asn Gln Asp Thr Leu Lys Cys Gly Ser Lys His Arg Arg Pro Thr
        595                 600                 605
Val Ser Ser Gln Phe Lys Val Asp Ser Leu His Ser Leu Met Ala Thr
    610                 615                 620
Leu Ser Ser Ser Asn Pro Phe Phe Val Arg Cys Ile Lys Pro Asn Met
625                 630                 635                 640
Gln Lys Met Pro Asp Gln Phe Asp Gln Ala Val Val Leu Asn Gln Leu
                645                 650                 655
Arg Tyr Ser Gly Met Leu Glu Thr Val Arg Ile Arg Lys Ala Gly Tyr
            660                 665                 670
Ala Val Arg Arg Pro Phe Gln Asp Phe Tyr Lys Arg Tyr Lys Val Leu
        675                 680                 685
Met Arg Asn Leu Ala Leu Pro Glu Asp Val Arg Gly Lys Cys Thr Ser
    690                 695                 700
Leu Leu Gln Leu Tyr Asp Ala Ser Asn Ser Glu Trp Gln Leu Gly Lys
705                 710                 715                 720
Thr Lys Val Phe Leu Arg Glu Ser Leu Glu Gln Lys Leu Glu Lys Arg
                725                 730                 735
Arg Glu Glu Glu Val Ser His Ala Ala Met Val Ile Arg Ala His Val
            740                 745                 750
Leu Gly Phe Leu Ala Arg Lys Gln Tyr Arg Lys Val Leu Tyr Cys Val
```

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        755                 760                 765

Val Ile Ile Gln Lys Asn Tyr Arg Ala Phe Leu Leu Arg Arg Arg Phe
    770                 775                 780

Leu His Leu Lys Lys Ala Ala Ile Val Phe Gln Lys Gln Leu Arg Gly
785                 790                 795                 800

Gln Ile Ala Arg Arg Val Tyr Arg Gln Leu Leu Ala Glu Lys Arg Glu
                805                 810                 815

Gln Glu Glu Lys Lys Lys Gln Glu Glu Glu Glu Lys Lys Lys Arg Glu
            820                 825                 830

Glu Glu Glu Arg Glu Arg Glu Arg Glu Arg Arg Glu Ala Glu Leu Arg
        835                 840                 845

Ala Gln Gln Glu Glu Glu Thr Arg Lys Gln Gln Glu Leu Glu Ala Leu
    850                 855                 860

Gln Lys Ser Gln Lys Glu Ala Glu Leu Thr Arg Glu Leu Glu Lys Gln
865                 870                 875                 880

Lys Glu Asn Lys Gln Val Glu Glu Ile Leu Arg Leu Glu Lys Glu Ile
                885                 890                 895

Glu Asp Leu Gln Arg Met Lys Glu Gln Gln Glu Leu Ser Leu Thr Glu
            900                 905                 910

Ala Ser Leu Gln Lys Leu Gln Glu Arg Arg Asp Gln Glu Leu Arg Arg
        915                 920                 925

Leu Glu Glu Glu Ala Cys Arg Ala Ala Gln Glu Phe Leu Glu Ser Leu
    930                 935                 940

Asn Phe Asp Glu Ile Asp Glu Cys Val Arg Asn Ile Glu Arg Ser Leu
945                 950                 955                 960

Ser Gly Gly Ser Glu Phe Ser Ser Glu Leu Ala Glu Ser Ala Cys Glu
                965                 970                 975

Glu Lys Pro Asn Phe Asn Phe Ser Gln Pro Tyr Pro Glu Glu Glu Val
            980                 985                 990

Asp Glu Gly Phe Glu Ala Asp Asp Asp Ala Phe Lys Asp Ser Pro Asn
        995                 1000                1005

Pro Ser  Glu His Gly His Ser  Asp Gln Arg Thr Ser  Gly Ile Arg
    1010                1015                1020

Thr Ser  Asp Asp Ser Ser Glu  Glu Asp Pro Tyr Met  Asn Asp Thr
    1025                1030                1035

Val Val  Pro Thr Ser Pro Ser  Ala Asp Ser Thr Val  Leu Leu Ala
    1040                1045                1050

Pro Ser  Val Gln Asp Ser Gly  Ser Leu His Asn Ser  Ser Ser Gly
    1055                1060                1065

Glu Ser  Thr Tyr Cys Met Pro  Gln Asn Ala Gly Asp  Leu Pro Ser
    1070                1075                1080

Pro Asp  Gly Asp Tyr Asp Tyr  Asp Gln Asp Asp Tyr  Glu Asp Gly
    1085                1090                1095

Ala Ile  Thr Ser Gly Ser Ser  Val Thr Phe Ser Asn  Ser Tyr Gly
```

1100 1105 1110

Ser Gln Trp Ser Pro Asp Tyr Arg Cys Ser Val Gly Thr Tyr Asn
1115 1120 1125

Ser Ser Gly Ala Tyr Arg Phe Ser Ser Glu Gly Ala Gln Ser Ser
1130 1135 1140

Phe Glu Asp Ser Glu Glu Asp Phe Asp Ser Arg Phe Asp Thr Asp
1145 1150 1155

Asp Glu Leu Ser Tyr Arg Arg Asp Ser Val Tyr Ser Cys Val Thr
1160 1165 1170

Leu Pro Tyr Phe His Ser Phe Leu Tyr Met Lys Gly Gly Leu Met
1175 1180 1185

Asn Ser Trp Lys Arg Arg Trp Cys Val Leu Lys Asp Glu Thr Phe
1190 1195 1200

Leu Trp Phe Arg Ser Lys Gln Glu Ala Leu Lys Gln Gly Trp Leu
1205 1210 1215

His Lys Lys Gly Gly Gly Ser Ser Thr Leu Ser Arg Arg Asn Trp
1220 1225 1230

Lys Lys Arg Trp Phe Val Leu Arg Gln Ser Lys Leu Met Tyr Phe
1235 1240 1245

Glu Asn Asp Ser Glu Glu Lys Leu Lys Gly Thr Val Glu Val Arg
1250 1255 1260

Thr Ala Lys Glu Ile Ile Asp Asn Thr Thr Lys Glu Asn Gly Ile
1265 1270 1275

Asp Ile Ile Met Ala Asp Arg Thr Phe His Leu Ile Ala Glu Ser
1280 1285 1290

Pro Glu Asp Ala Ser Gln Trp Phe Ser Val Leu Ser Gln Val His
1295 1300 1305

Ala Ser Thr Asp Gln Glu Ile Gln Glu Met His Asp Glu Gln Ala
1310 1315 1320

Asn Pro Gln Asn Ala Val Gly Thr Leu Asp Val Gly Leu Ile Asp
1325 1330 1335

Ser Val Cys Ala Ser Asp Ser Pro Asp Arg Pro Asn Ser Phe Val
1340 1345 1350

Ile Ile Thr Ala Asn Arg Val Leu His Cys Asn Ala Asp Thr Pro
1355 1360 1365

Glu Glu Met His His Trp Ile Thr Leu Leu Gln Arg Ser Lys Gly
1370 1375 1380

Asp Thr Arg Val Glu Gly Gln Glu Phe Ile Val Arg Gly Trp Leu
1385 1390 1395

His Lys Glu Val Lys Asn Ser Pro Lys Met Ser Ser Leu Lys Leu
1400 1405 1410

Lys Lys Arg Trp Phe Val Leu Thr His Asn Ser Leu Asp Tyr Tyr
1415 1420 1425

Lys Ser Ser Glu Lys Asn Ala Leu Lys Leu Gly Thr Leu Val Leu

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    1430                1435                1440

Asn Ser Leu Cys Ser Val Val Pro Pro Asp Glu Lys Ile Phe Lys
    1445                1450                1455

Glu Thr Gly Tyr Trp Asn Val Thr Val Tyr Gly Arg Lys His Cys
    1460                1465                1470

Tyr Arg Leu Tyr Thr Lys Leu Leu Asn Glu Ala Thr Arg Trp Ser
    1475                1480                1485

Ser Val Ile Gln Asn Val Thr Asp Thr Lys Ala Pro Ile Asp Thr
    1490                1495                1500

Pro Thr Gln Gln Leu Ile Gln Asp Ile Lys Glu Asn Cys Leu Asn
    1505                1510                1515

Ser Asp Val Val Glu Gln Ile Tyr Lys Arg Asn Pro Ile Leu Arg
    1520                1525                1530

Tyr Thr His His Pro Leu His Ser Pro Leu Leu Pro Leu Pro Tyr
    1535                1540                1545

Gly Asp Ile Asn Leu Asn Leu Leu Lys Asp Lys Gly Tyr Thr Thr
    1550                1555                1560

Leu Gln Asp Glu Ala Ile Lys Ile Phe Asn Ser Leu Gln Gln Leu
    1565                1570                1575

Glu Ser Met Ser Asp Pro Ile Pro Ile Ile Gln Gly Ile Leu Gln
    1580                1585                1590

Thr Gly His Asp Leu Arg Pro Leu Arg Asp Glu Leu Tyr Cys Gln
    1595                1600                1605

Leu Ile Lys Gln Thr Asn Lys Val Pro His Pro Gly Ser Val Gly
    1610                1615                1620

Asn Leu Tyr Ser Trp Gln Ile Leu Thr Cys Leu Ser Cys Thr Phe
    1625                1630                1635

Leu Pro Ser Arg Gly Ile Leu Lys Tyr Leu Lys Phe His Leu Lys
    1640                1645                1650

Arg Ile Arg Glu Gln Phe Pro Gly Thr Glu Met Glu Lys Tyr Ala
    1655                1660                1665

Leu Phe Thr Tyr Glu Ser Leu Lys Lys Thr Lys Cys Arg Glu Phe
    1670                1675                1680

Val Pro Ser Arg Asp Glu Ile Glu Ala Leu Ile His Arg Gln Glu
    1685                1690                1695

Met Thr Ser Thr Val Tyr Cys His Gly Gly Gly Ser Cys Lys Ile
    1700                1705                1710

Thr Ile Asn Ser His Thr Thr Ala Gly Glu Val Val Glu Lys Leu
    1715                1720                1725

Ile Arg Gly Leu Ala Met Glu Asp Ser Arg Asn Met Phe Ala Leu
    1730                1735                1740

Phe Glu Tyr Asn Gly His Val Asp Lys Ala Ile Glu Ser Arg Thr
    1745                1750                1755

Val Val Ala Asp Val Leu Ala Lys Phe Glu Lys Leu Ala Ala Thr
```

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    1760                1765                1770
Ser Glu Val Gly Asp Leu Pro Trp Lys Phe Tyr Phe Lys Leu Tyr
    1775                1780                1785
Cys Phe Leu Asp Thr Asp Asn Val Pro Lys Asp Ser Val Glu Phe
    1790                1795                1800
Ala Phe Met Phe Glu Gln Ala His Glu Ala Val Ile His Gly His
    1805                1810                1815
His Pro Ala Pro Glu Glu Asn Leu Gln Val Leu Ala Ala Leu Arg
    1820                1825                1830
Leu Gln Tyr Leu Gln Gly Asp Tyr Thr Leu His Ala Ala Ile Pro
    1835                1840                1845
Pro Leu Glu Glu Val Tyr Ser Leu Gln Arg Leu Lys Ala Arg Ile
    1850                1855                1860
Ser Gln Ser Thr Lys Thr Phe Thr Pro Cys Glu Arg Leu Glu Lys
    1865                1870                1875
Arg Arg Thr Ser Phe Leu Glu Gly Thr Leu Arg Arg Ser Phe Arg
    1880                1885                1890
Thr Gly Ser Val Val Arg Gln Lys Val Glu Glu Glu Gln Met Leu
    1895                1900                1905
Asp Met Trp Ile Lys Glu Glu Val Ser Ser Ala Arg Ala Ser Ile
    1910                1915                1920
Ile Asp Lys Trp Arg Lys Phe Gln Gly Met Asn Gln Glu Gln Ala
    1925                1930                1935
Met Ala Lys Tyr Met Ala Leu Ile Lys Glu Trp Pro Gly Tyr Gly
    1940                1945                1950
Ser Thr Leu Phe Asp Val Glu Cys Lys Glu Gly Gly Phe Pro Gln
    1955                1960                1965
Glu Leu Trp Leu Gly Val Ser Ala Asp Ala Val Ser Val Tyr Lys
    1970                1975                1980
Arg Gly Glu Gly Arg Pro Leu Glu Val Phe Gln Tyr Glu His Ile
    1985                1990                1995
Leu Ser Phe Gly Ala Pro Leu Ala Asn Thr Tyr Lys Ile Val Val
    2000                2005                2010
Asp Glu Arg Glu Leu Leu Phe Glu Thr Ser Glu Val Val Asp Val
    2015                2020                2025
Ala Lys Leu Met Lys Ala Tyr Ile Ser Met Ile Val Lys Lys Arg
    2030                2035                2040
Tyr Ser Thr Thr Arg Ser Ala Ser Ser Gln Gly Ser Ser Arg
    2045                2050                2055
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Table 11 hMX2 nucleotide sequence (SEQ ID NO:11)

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agctagtatc ttttattgtc agaacttctg tgagccaaca aacagttttg catggttgta    60
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cacaaaggga caaggcaaat ttctttttc gtgtgggtag acttagttgg cccaagtcct   120
taaaactttt ccatataaaa ataaaaagtc caagaccaga ttatttttct tctggtcata   180
aatgctgatt tatttacagg tgccttgttc agaccaccat tataaacttg ggataaaata   240
tgtgtgtatt aaagcctcag catttaatgt cagggtcctt tgaagattca ctcaagtgtt   300
aagacgtttc tggaatgcag cgtctctccc ccatagtcaa catggttatt atatctgtaa   360
tctatccaga atgatagaag ctaaccttcc aagtaacact ttgtttttaa cttaaatctt   420
ttagacatga aagactccaa aatgacttca ttcttgttct aaaaccagca ctggagccag   480
ctgttgaaga gtggtttata aatacagtta tcttgtaggc tgcttatctg tttataatac   540
agcagacaca gatggcagac tttgctacat gtaaaacaat ggagtcaaca cgtgtttttc   600
aaaatacagc aaagacagga aaatccagga tttgggtttg ttaataaaac caccttataa   660
agtaacaatt gagactatag ctctgcatta ttaaaatata cagactgtgt acaccattac   720
acatcctttt tccctttgct ttttaatgct catgaaacca tgattaaggt gttgagttta   780
tgaacacatg cacgaacagg caagcacgta cacttaaaag atgaaacaaa gaaaaaagtt   840
gattcatgtc attccatgag aaaggctgcc cgcagcactc cagctcaaac acactgtccc   900
ctcgagctct ccatcccccc tcccactccc tcaccttccc tcagattcgg ggaaatcagg   960
ttgggaggtt agtgcatcat tgacagagaa tgccccccct ccacgctctg ttaagtctcc  1020
cccagaaggg ggaaaggcag ttcccttcag tagcacagtt acggtcgatt agtgttggtt  1080
ccacaagtta aggcacttcc ggctgctttg gtggcagcgt ggttcctccc ctccttttt   1140
aaggcatgtg tcctctaaga gtagtaaagc tttggaaact gtgcagactg ttaaagttga  1200
cagcttaata caggatcaat gaaggcggca ggcaaaagga tcctcggaga cacctccctc  1260
agaccagaag cttccagaaa gcctgggcag ctctgtgttt gttttggctg ggcatggcac  1320
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tcccgccttc acctggagct gccctggctg ctggcggagc gtgtcgtgct gtagcgcttc  1440
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tcaaagagca gctccctctc atcgaccacg atcttatacg tattcgccag gggtgcccca  1560
aaagagagga tgtgttcata ctggaagact tccagtggtc ttccctctcc acgcttgtag  1620
acggagacgg cgtccgcgct gacacccaac cagagttcct gagggaagcc accttccttg  1680
cactggtggg caagagtcaa cagaagagtt aagtcatgaa gtggttggca acagaaagca  1740
tctaaaccat aagacaggct ttgagtgaag tcctctgtgc agaagattaa atatattcga  1800
tgtgcatgca tgcatggagg ggcctgaaat atgaaaaatg gcacctctct ggctatcttg  1860
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tcttgctttg actctccact tctcagcatt attctactag ctgtttggat tagctacgtg  1980
gaagtggcct ggaaacgtac atgcttggcc gggggactta agaaagcttc cctgcaaccc  2040
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gttagtcttc aaatacaaaa tctaggatca cagaggaaaa ttctccaaat cacgcatgct  2160
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gatctcctga cctcatgatc cgcccgcctt ggcctcccaa agcgctggga ttacaggcat  2700
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gagccaccgc gcccggccaa gccagtagct ttctatgcta attcacagct cacgttttgc   2760
aggaagccaa gagtttaact gctattatct attccttgtc agggagaaat ggaattatgg   2820
ctttgtacaa agcacctgat ttttttatac ttaaaaacag gcataattga accaaccaaa   2880
ccaatcaaaa acatcaccta atgaaaagcc acccacggat tctagaattt ataatattta   2940
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aaaatggaag ctaatctaga cgatgagctg gcacacttat ctgttaaggg ctgcatagta   3060
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aaacataaat gcaaactcca cactgtcttt tggcacgttg tctgtgtcca ggaagcagta   4260
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aaacttggct aagacatcag ctacgacggt tcgactttca atggctttgt cgacgtggcc   4380
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tcgggaaggc acaaactctc ggcatttggt tttcttaaga gattcgtaag tgaagagagc   4620
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ctcatcctga agggtggtat agcctttgtc tttcagcaag ttgagattta tgtccccata   4980
cggaaggggc aggagcgggg agtgcaaggg gtgatgggtg tatcgaagga tcgggttccg   5040
cttgtaaatc tgttccacca catccgagtt caggcagttc tccttgatat cttgaatcag   5100
ctgctgggtg ggggtgtcga tcggggcctt ggtgtcagtc acgttttgaa tgacactgga   5160
ccaccgggtg gcctcgttga gcagcttggt gtagagccgg taacagtgct tgcgcccgta   5220
cacggtgacg ttccagtagc ctgtctcttt gaatatcttc tcatctgggg ggacgacaga   5280
gcagaggctg ttgaggacca gggtccccag tttgagcgcg ttcttctctg aactcttgta   5340
```

gtaatccagg gaattgtggg tgagtacaaa ccaccgtttc ttcagtttca gtgaagacat 5400
ctttggactg ttcttcacct ctttgtgcaa ccatcctctc acgatgaatt cctggccctc 5460
cactctggtg tccccttttgg acctctgcag cagggttatc cagtggtgca tctcctccgg 5520
cgtgtcggcg ttgcagtgca gcacccggtt ggccgtgatg atcacaaacg agttgggtct 5580
atcagggctg tcagaggcac acacagaatc aatcagcccc acatccaagg tgcccacagc 5640
attctgtggg tttgcctgct catcatgcat ctcctggatc tcctggtccg tggacgcgtg 5700
gacctgactc agcacgctga accactggct ggcatcttct ggggactctg caatcaggtg 5760
gaaagtccta tcggccataa tgatgtcgat cccattctcc ttggtggtgt tatctatgat 5820
ctcttttgcc gttcgcactt ctacggtgcc cttgagcttc tcctcgctgt cgttttcaaa 5880
gtacatcagc ttggactggc ggaggacaaa ccagcgcttc ttccaatttc tcctggacag 5940
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gcggaaccac aagaaggttt catccttgag gacgcaccag cggcgtttcc aagagttcat 6060
caggccacct ttcatgtaca gaaagctgtg gaaatacggc agagtgacac agctgtacac 6120
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caggtgcaaa aatctcctcc tcagaaggaa tgctctgtaa ttcttctgta ttatcaccac 7320
acaataaagg acctttctgt attgtttccg tgctaagaag cccaagacat gggcccgaat 7380
caccatggcc gcgtggctca cttcctcttc cctccgcttc tccagtttct gttccaagga 7440
ttctcgaaga aataccttgg tcttccccag ctgccactcg ctgttggagg catcatagag 7500
ctgcagcagg ctcgtgcact tccctcggac gtcctcaggc agagccagat tcctcatcag 7560
cactttatac cttttgtaaa agtcctgaaa gggtcttcgg accgcatacc cagctttgcg 7620
gattctcaca gtctccagca tccctgagta ccgcagctgg ttcagcacaa ccgcctggtc 7680
aaactggtct ggcatcttct gcatgtttgg cttgatacag cgaacaaaga aaggattaga 7740
ggagcttagc gttgccatta aggaatgcag tgagtcaacc ttgaactgtg agctgactgt 7800
aggccgccga tgtttgcttc cacatttcaa ggtatcctgg ttgttgcggc ttgaaacatg 7860
ttcaaaaaga tcgtagataa agtcaaaccg gctttctctt agcaaattga gaaggtcatc 7920
tcgaaatgta tctctgttct tctccaagat acctcggaca tcatattgca cctctccagc 7980

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cgcatgctga ctgtgtagct tctccaataa ggtgctgtct gtggcttgag gaaaatggct    8100
ttcttcattg ataagggcta ggaggccaag tttcttctca atcaagtcca ggcattctcc    8160
attgtctatc cagtcaatat cttcccacac taatccttcc ctgctatatt ctagttgttc    8220
taaagaaaaa atatgcttgt tgaagtactc ctgaagtttc tcgtttgcat agtttatatt    8280
gaactgttca aagtgattaa cctcaaagtt ttcaaatcca aagatgtcga ggatgccaat    8340
agacttgaag tcctcattgc ctttgatcct gctgttgatc ttcttgatta cccactcaaa    8400
gcagcacgca tacagagcca tggccaggga gtccctgctg tctactgcct gttgaacatt    8460
gagaggcgtg aggatctctt ctcccctgag gaacattgat ctctgggtca aagcatctgt    8520
gagctgtgtt gggtccagcc caagtaactc cgcagatctg cccaaagctg ttttgaagga    8580
aacctgtgcc ccaccagcag tgataaattc tatgttccca agatgcagta taccagcaag    8640
cagcctcgac acttcccgaa cttcctcctt gctgaactgc atcacgtcca ttgccgtaat    8700
aacttcccta aaggattcct ggtcactgat tgtcttgtct tctacacatc cagactgatt    8760
caagtagtgg tagttttctg gcgtagataa ataaaattct tctctttctt catgttccag    8820
ccctgccagc agtgcataaa atatgtgata attcctttcc ccgggatttt gccttactac    8880
tcggttctgg gaagagagga tacaatctac aattctcccg ccctgaatat ttcctttctg    8940
acagatgttc agctgaacaa acttcccaaa gcgactagag ttgttgttgt acacggtctt    9000
cgcattgccg aaagcttcca tgatggggct gctttcaaga atagctcgtt caacacagga    9060
tgtcttctcc tttaaggaca attccaaaga ctgttgactg atgactgaca gaaacttgag    9120
gatcaattta gtgctttcgg ttttacctgc cccactttca cccttgatga ggatgcactg    9180
gttgtcgtgg cgcttccaca ggcagcggta gcactcgttg gcgatggcga agatgtgcgg    9240
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ggcgatgggc tggtaggggt tcacagaggc caggatggag ccgatgtagg tccatatttg    9360
atttctctta taccgctgga ataagttata catgatggag ccgccatgga gctctgtcaa    9420
ggacgccatg tcatccacgc cctcctcgtt cgtggggtgc atagcagtca ccttctggtg    9480
ggtaattgtg ctctgcttgt aagtgaatac ctgaccatag tctgtccgga agacgacgat    9540
gccttctgca caggaattta cagtacttgg aaaatgctgg ccatttctc tcagccagac    9600
ccgtgttccc tgtaaacaaa a                                              9621
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Table 12 hMX2 polypeptide sequence (SEQ ID NO:12)

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Phe Cys Leu Gln Gly Thr Arg Val Trp Leu Arg Glu Asn Gly Gln His
1               5                  10                  15

Phe Pro Ser Thr Val Asn Ser Cys Ala Glu Gly Ile Val Val Phe Arg
            20                  25                  30

Thr Asp Tyr Gly Gln Val Phe Thr Tyr Lys Gln Ser Thr Ile Thr His
        35                  40                  45

Gln Lys Val Thr Ala Met His Pro Thr Asn Glu Glu Gly Val Asp Asp
    50                  55                  60

Met Ala Ser Leu Thr Glu Leu His Gly Gly Ser Ile Met Tyr Asn Leu
65                  70                  75                  80

Phe Gln Arg Tyr Lys Arg Asn Gln Ile Trp Thr Tyr Ile Gly Ser Ile
                85                  90                  95

Leu Ala Ser Val Asn Pro Tyr Gln Pro Ile Ala Gly Leu Tyr Glu Pro
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                100                 105                 110

Ala Thr Met Glu Gln Tyr Ser Arg Arg His Leu Gly Glu Leu Pro Pro
        115                 120                 125

His Ile Phe Ala Ile Ala Asn Glu Cys Tyr Arg Cys Leu Trp Lys Arg
    130                 135                 140

His Asp Asn Gln Cys Ile Leu Ile Lys Gly Glu Ser Gly Ala Gly Lys
145                 150                 155                 160

Thr Glu Ser Thr Lys Leu Ile Leu Lys Phe Leu Ser Val Ile Ser Gln
                165                 170                 175

Gln Ser Leu Glu Leu Ser Leu Lys Glu Lys Thr Ser Cys Val Glu Arg
            180                 185                 190

Ala Ile Leu Glu Ser Ser Pro Ile Met Glu Ala Phe Gly Asn Ala Lys
        195                 200                 205

Thr Val Tyr Asn Asn Asn Ser Ser Arg Phe Gly Lys Phe Val Gln Leu
    210                 215                 220

Asn Ile Cys Gln Lys Gly Asn Ile Gln Gly Gly Arg Ile Val Asp Cys
225                 230                 235                 240

Ile Leu Ser Ser Gln Asn Arg Val Val Arg Gln Asn Pro Gly Glu Arg
                245                 250                 255

Asn Tyr His Ile Phe Tyr Ala Leu Leu Ala Gly Leu Glu His Glu Glu
            260                 265                 270

Arg Glu Glu Phe Tyr Leu Ser Thr Pro Glu Asn Tyr His Tyr Leu Asn
        275                 280                 285

Gln Ser Gly Cys Val Glu Asp Lys Thr Ile Ser Asp Gln Glu Ser Phe
    290                 295                 300

Arg Glu Val Ile Thr Ala Met Asp Val Met Gln Phe Ser Lys Glu Glu
305                 310                 315                 320

Val Arg Glu Val Ser Arg Leu Leu Ala Gly Ile Leu His Leu Gly Asn
                325                 330                 335

Ile Glu Phe Ile Thr Ala Gly Gly Ala Gln Val Ser Phe Lys Thr Ala
            340                 345                 350

Leu Gly Arg Ser Ala Glu Leu Leu Gly Leu Asp Pro Thr Gln Leu Thr
        355                 360                 365

Asp Ala Leu Thr Gln Arg Ser Met Phe Leu Arg Gly Glu Glu Ile Leu
    370                 375                 380

Thr Pro Leu Asn Val Gln Gln Ala Val Asp Ser Arg Asp Ser Leu Ala
385                 390                 395                 400

Met Ala Leu Tyr Ala Cys Cys Phe Glu Trp Val Ile Lys Lys Ile Asn
                405                 410                 415

Ser Arg Ile Lys Gly Asn Glu Asp Phe Lys Ser Ile Gly Ile Leu Asp
            420                 425                 430

Ile Phe Gly Phe Glu Asn Phe Glu Val Asn His Phe Glu Gln Phe Asn
        435                 440                 445

Ile Asn Tyr Ala Asn Glu Lys Leu Gln Glu Tyr Phe Asn Lys His Ile
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    450                 455                 460
Phe Ser Leu Glu Gln Leu Glu Tyr Ser Arg Glu Gly Leu Val Trp Glu
465                 470                 475                 480
Asp Ile Asp Trp Ile Asp Asn Gly Glu Cys Leu Asp Leu Ile Glu Lys
                485                 490                 495
Lys Leu Gly Leu Leu Ala Leu Ile Asn Glu Glu Ser His Phe Pro Gln
            500                 505                 510
Ala Thr Asp Ser Thr Leu Leu Glu Lys Leu His Ser Gln His Ala Asn
        515                 520                 525
Asn His Phe Tyr Val Lys Pro Arg Val Ala Val Asn Asn Phe Gly Val
    530                 535                 540
Lys His Tyr Ala Gly Glu Val Gln Tyr Asp Val Arg Gly Ile Leu Glu
545                 550                 555                 560
Lys Asn Arg Asp Thr Phe Arg Asp Asp Leu Leu Asn Leu Leu Arg Glu
                565                 570                 575
Ser Arg Phe Asp Phe Ile Tyr Asp Leu Phe Glu His Val Ser Ser Arg
            580                 585                 590
Asn Asn Gln Asp Thr Leu Lys Cys Gly Ser Lys His Arg Arg Pro Thr
        595                 600                 605
Val Ser Ser Gln Phe Lys Val Asp Ser Leu His Ser Leu Met Ala Thr
    610                 615                 620
Leu Ser Ser Ser Asn Pro Phe Phe Val Arg Cys Ile Lys Pro Asn Met
625                 630                 635                 640
Gln Lys Met Pro Asp Gln Phe Asp Gln Ala Val Val Leu Asn Gln Leu
                645                 650                 655
Arg Tyr Ser Gly Met Leu Glu Thr Val Arg Ile Arg Lys Ala Gly Tyr
            660                 665                 670
Ala Val Arg Arg Pro Phe Gln Asp Phe Tyr Lys Arg Tyr Lys Val Leu
        675                 680                 685
Met Arg Asn Leu Ala Leu Pro Glu Asp Val Arg Gly Lys Cys Thr Ser
    690                 695                 700
Leu Leu Gln Leu Tyr Asp Ala Ser Asn Ser Glu Trp Gln Leu Gly Lys
705                 710                 715                 720
Thr Lys Val Phe Leu Arg Glu Ser Leu Glu Gln Lys Leu Glu Lys Arg
                725                 730                 735
Arg Glu Glu Glu Val Ser His Ala Ala Met Val Ile Arg Ala His Val
            740                 745                 750
Leu Gly Phe Leu Ala Arg Lys Gln Tyr Arg Lys Val Leu Tyr Cys Val
        755                 760                 765
Val Ile Ile Gln Lys Asn Tyr Arg Ala Phe Leu Leu Arg Arg Arg Phe
    770                 775                 780
Leu His Leu Lys Lys Ala Ala Ile Val Phe Gln Lys Gln Leu Arg Gly
785                 790                 795                 800
Gln Ile Ala Arg Arg Val Tyr Arg Gln Leu Leu Ala Glu Lys Arg Glu
```

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                805                 810                 815

Gln Glu Glu Lys Lys Lys Gln Glu Glu Glu Glu Lys Lys Lys Arg Glu
            820                 825                 830

Glu Glu Glu Arg Glu Arg Glu Arg Glu Arg Arg Glu Ala Glu Leu Arg
        835                 840                 845

Ala Gln Gln Glu Glu Glu Thr Arg Lys Gln Gln Glu Leu Glu Ala Leu
    850                 855                 860

Gln Lys Ser Gln Lys Glu Ala Glu Leu Thr Arg Glu Leu Glu Lys Gln
865                 870                 875                 880

Lys Glu Asn Lys Gln Val Glu Glu Ile Leu Arg Leu Glu Lys Glu Ile
                885                 890                 895

Glu Asp Leu Gln Arg Met Lys Glu Gln Gln Glu Leu Ser Leu Thr Glu
            900                 905                 910

Ala Ser Leu Gln Lys Leu Gln Glu Arg Arg Asp Gln Glu Leu Arg Arg
        915                 920                 925

Leu Glu Glu Glu Ala Cys Arg Ala Ala Gln Glu Phe Leu Glu Ser Leu
    930                 935                 940

Asn Phe Asp Glu Ile Asp Glu Cys Val Arg Asn Ile Glu Arg Ser Leu
945                 950                 955                 960

Ser Gly Gly Ser Glu Phe Ser Ser Glu Leu Ala Glu Ser Ala Cys Glu
                965                 970                 975

Glu Lys Pro Asn Phe Asn Phe Ser Gln Pro Tyr Pro Glu Glu Glu Val
            980                 985                 990

Asp Glu Gly Phe Glu Ala Asp Asp  Asp Ala Phe Lys Asp  Ser Pro Asn
        995                 1000                1005

Pro Ser  Glu His Gly His Ser  Asp Gln Arg Thr Ser  Gly Ile Arg
    1010                1015                1020

Thr Ser  Asp Asp Ser Ser Glu  Glu Asp Pro Tyr Met  Asn Asp Thr
    1025                1030                1035

Val Val  Pro Thr Ser Pro Ser  Ala Asp Ser Thr Val  Leu Leu Ala
    1040                1045                1050

Pro Ser  Val Gln Asp Ser Gly  Ser Leu His Asn Ser  Ser Ser Gly
    1055                1060                1065

Glu Ser  Thr Tyr Cys Met Pro  Gln Asn Ala Gly Asp  Leu Pro Ser
    1070                1075                1080

Pro Asp  Gly Asp Tyr Asp Tyr  Asp Gln Asp Asp Tyr  Glu Asp Gly
    1085                1090                1095

Ala Ile  Thr Ser Gly Ser Ser  Val Thr Phe Ser Asn  Ser Tyr Gly
    1100                1105                1110

Ser Gln  Trp Ser Pro Asp Tyr  Arg Cys Ser Val Gly  Thr Tyr Asn
    1115                1120                1125

Ser Ser  Gly Ala Tyr Arg Phe  Ser Ser Glu Gly Ala  Gln Ser Ser
    1130                1135                1140

Phe Glu  Asp Ser Glu Glu Asp  Phe Asp Ser Arg Phe  Asp Thr Asp
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1145 1150 1155

Asp Glu Leu Ser Tyr Arg Arg Asp Ser Val Tyr Ser Cys Val Thr
1160 1165 1170

Leu Pro Tyr Phe His Ser Phe Leu Tyr Met Lys Gly Gly Leu Met
1175 1180 1185

Asn Ser Trp Lys Arg Arg Trp Cys Val Leu Lys Asp Glu Thr Phe
1190 1195 1200

Leu Trp Phe Arg Ser Lys Gln Glu Ala Leu Lys Gln Gly Trp Leu
1205 1210 1215

His Lys Lys Gly Gly Gly Ser Ser Thr Leu Ser Arg Arg Asn Trp
1220 1225 1230

Lys Lys Arg Trp Phe Val Leu Arg Gln Ser Lys Leu Met Tyr Phe
1235 1240 1245

Glu Asn Asp Ser Glu Glu Lys Leu Lys Gly Thr Val Glu Val Arg
1250 1255 1260

Thr Ala Lys Glu Ile Ile Asp Asn Thr Thr Lys Glu Asn Gly Ile
1265 1270 1275

Asp Ile Ile Met Ala Asp Arg Thr Phe His Leu Ile Ala Glu Ser
1280 1285 1290

Pro Glu Asp Ala Ser Gln Trp Phe Ser Val Leu Ser Gln Val His
1295 1300 1305

Ala Ser Thr Asp Gln Glu Ile Gln Glu Met His Asp Glu Gln Ala
1310 1315 1320

Asn Pro Gln Asn Ala Val Gly Thr Leu Asp Val Gly Leu Ile Asp
1325 1330 1335

Ser Val Cys Ala Ser Asp Ser Pro Asp Arg Pro Asn Ser Phe Val
1340 1345 1350

Ile Ile Thr Ala Asn Arg Val Leu His Cys Asn Ala Asp Thr Pro
1355 1360 1365

Glu Glu Met His His Trp Ile Thr Leu Leu Gln Arg Ser Lys Gly
1370 1375 1380

Asp Thr Arg Val Glu Gly Gln Glu Phe Ile Val Arg Gly Trp Leu
1385 1390 1395

His Lys Glu Val Lys Asn Ser Pro Lys Met Ser Ser Leu Lys Leu
1400 1405 1410

Lys Lys Arg Trp Phe Val Leu Thr His Asn Ser Leu Asp Tyr Tyr
1415 1420 1425

Lys Ser Ser Glu Lys Asn Ala Leu Lys Leu Gly Thr Leu Val Leu
1430 1435 1440

Asn Ser Leu Cys Ser Val Val Pro Pro Asp Glu Lys Ile Phe Lys
1445 1450 1455

Glu Thr Gly Tyr Trp Asn Val Thr Val Tyr Gly Arg Lys His Cys
1460 1465 1470

Tyr Arg Leu Tyr Thr Lys Leu Leu Asn Glu Ala Thr Arg Trp Ser

1475 1480 1485

Ser Val Ile Gln Asn Val Thr Asp Thr Lys Ala Pro Ile Asp Thr
1490 1495 1500

Pro Thr Gln Gln Leu Ile Gln Asp Ile Lys Glu Asn Cys Leu Asn
1505 1510 1515

Ser Asp Val Val Glu Gln Ile Tyr Lys Arg Asn Pro Ile Leu Arg
1520 1525 1530

Tyr Thr His His Pro Leu His Ser Pro Leu Leu Pro Leu Pro Tyr
1535 1540 1545

Gly Asp Ile Asn Leu Asn Leu Leu Lys Asp Lys Gly Tyr Thr Thr
1550 1555 1560

Leu Gln Asp Glu Ala Ile Lys Ile Phe Asn Ser Leu Gln Gln Leu
1565 1570 1575

Glu Ser Met Ser Asp Pro Ile Pro Ile Ile Gln Gly Ile Leu Gln
1580 1585 1590

Thr Gly His Asp Leu Arg Pro Leu Arg Asp Glu Leu Tyr Cys Gln
1595 1600 1605

Leu Ile Lys Gln Thr Asn Lys Val Pro His Pro Gly Ser Val Gly
1610 1615 1620

Asn Leu Tyr Ser Trp Gln Ile Leu Thr Cys Leu Ser Cys Thr Phe
1625 1630 1635

Leu Pro Ser Arg Gly Ile Leu Lys Tyr Leu Lys Phe His Leu Lys
1640 1645 1650

Arg Ile Arg Glu Gln Phe Pro Gly Thr Glu Met Glu Lys Tyr Ala
1655 1660 1665

Leu Phe Thr Tyr Glu Ser Leu Lys Lys Thr Lys Cys Arg Glu Phe
1670 1675 1680

Val Pro Ser Arg Asp Glu Ile Glu Ala Leu Ile His Arg Gln Glu
1685 1690 1695

Met Thr Ser Thr Val Tyr Cys His Gly Gly Gly Ser Cys Lys Ile
1700 1705 1710

Thr Ile Asn Ser His Thr Thr Ala Gly Glu Val Val Glu Lys Leu
1715 1720 1725

Ile Arg Gly Leu Ala Met Glu Asp Ser Arg Asn Met Phe Ala Leu
1730 1735 1740

Phe Glu Tyr Asn Gly His Val Asp Lys Ala Ile Glu Ser Arg Thr
1745 1750 1755

Val Val Ala Asp Val Leu Ala Lys Phe Glu Lys Leu Ala Ala Thr
1760 1765 1770

Ser Glu Val Gly Asp Leu Pro Trp Lys Phe Tyr Phe Lys Leu Tyr
1775 1780 1785

Cys Phe Leu Asp Thr Asp Asn Val Pro Lys Asp Ser Val Glu Phe
1790 1795 1800

Ala Phe Met Phe Glu Gln Ala His Glu Ala Val Ile His Gly His

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    1805                1810                1815

His Pro  Ala Pro Glu Glu Asn  Leu Gln Val Leu Ala  Ala Leu Arg
    1820                1825                1830

Leu Gln  Tyr Leu Gln Gly Asp  Tyr Thr Leu His Ala  Ala Ile Pro
    1835                1840                1845

Pro Leu  Glu Glu Val Tyr Ser  Leu Gln Arg Leu Lys  Ala Arg Ile
    1850                1855                1860

Ser Gln  Ser Thr Lys Thr Phe  Thr Pro Cys Glu Arg  Leu Glu Lys
    1865                1870                1875

Arg Arg  Thr Ser Phe Leu Glu  Gly Thr Leu Arg Arg  Ser Phe Arg
    1880    .           1885                1890

Thr Gly  Ser Val Val Arg Gln  Lys Val Glu Glu Glu  Gln Met Leu
    1895                1900                1905

Asp Met  Trp Ile Lys Glu Glu  Val Ser Ser Ala Arg  Ala Ser Ile
    1910                1915                1920

Ile Asp  Lys Trp Arg Lys Phe  Gln Gly Met Asn Gln  Glu Gln Ala
    1925                1930                1935

Met Ala  Lys Tyr Met Ala Leu  Ile Lys Glu Trp Pro  Gly Tyr Gly
    1940                1945                1950

Ser Thr  Leu Phe Asp Val Glu  Val Arg Thr Gly Cys  His Val Leu
    1955                1960                1965

Gly Trp  Ala Gly Cys Trp His  Leu Arg Thr Trp Ile  Thr Ala Lys
    1970                1975                1980

Phe Met  Trp Arg Glu Asp Lys  Met Glu His Phe Ala  Leu Ser Thr
    1985                1990                1995

Ser Phe  Phe Arg Ala Pro Lys  Ile Val Pro Leu Thr  Pro Pro Phe
    2000                2005                2010

Ser Ser  Gln Phe Leu Phe Ser  Cys Val Val Asn Ala  Ser Val Ile
    2015                2020                2025

Leu Gly  Met Asn Ala Lys Leu  Arg Cys His Leu Phe  Phe Tyr Pro
    2030                2035                2040

Ser Leu  Gly Lys Leu
    2045
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Table 13 hMP nucleotide sequence (SEQ ID NO:13)

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ccaacttttg cagctccacc caggatgtgg cctcgctcca ccccagctgt gcgcctctct     60
ccacccctag gcgaaggcac tagaatttcc caaattaaga acgaagagga agtttggacc    120
ttttcggcca ccgctcgctt caatatggct gcccccaggg agagacgagg ctaccatgaa    180
ggagccgagc gcagaccctg agtccgtcac ccatggatcg cagcgcggag ttcaggaaat    240
ggaaggcgca atgtttgagc aaagcggacc tcagccggaa gggcagtgtt gacgaggatg    300
tggtagagct tgtgcagttt ctgaacatgc gagatcagtt tttcaccacc agctccttcg    360
ctggccgcat cctactcctt gaccggggta taaatggttt tgaggttcag aaacaaaact    420
gttgctggct actggttaca cacaaacttt gtgtaaaaga tgatgtgatt gtagctctga    480
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agaaagcaaa tggtgatgcc actttgaaat ttgaaccatt tgttcttcat gtgcagtgtc   540
gacaattgca ggatgcacag attctgcatt ccatggcaat agattctggt ttcaggaact   600
ctggcataac ggtgggaaag agaggaaaaa ctatgttggc tgtccggagt acacatggct   660
tagaagttcc attaagccat aagggaaaac tgatggtgac agaggaatat attgacttcc   720
tgttaaatgt ggcaaatcaa aaaatggagg aaaacaagaa aagaattgag aggttttaca   780
actgcctaca gcatgctttg gaaagggaaa cgatgactaa cttacatccc aagatcaaag   840
agaaaaataa ctcatcatat attcataaga aaaaaagaaa cccagaaaaa acacgtgccc   900
agtgtattac taaagaaagt gatgaagaac ttgaaaatga tgatgatgat gatctaggaa   960
tcaatgttac catcttccct gaagattact aagctttggt tctgatgtgt cttggccgta  1020
atgtttctag taggttttat aaagctgctc ttcataagag tattttagtt tgttgagtgt  1080
atcagccatt cataagccag taatgacaag tgcagagctt caaactataa ctttgttgcc  1140
cagaggatgt gcagttgtca tctaagctct cagcagtacc cggcttatcc tacgacttca  1200
cctgaaatgc tatagttatc cctacttttt taccagtttc tcccagaagc acctgcttaa  1260
taaatcaaag atgtttgaaa aaaaaaaa                                     1288
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Table 14 hMP polypeptide sequence (SEQ ID NO:14)

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Met Asp Arg Ser Ala Glu Phe Arg Lys Trp Lys Ala Gln Cys Leu Ser
1               5                  10                  15

Lys Ala Asp Leu Ser Arg Lys Gly Ser Val Asp Glu Asp Val Val Glu
            20                  25                  30

Leu Val Gln Phe Leu Asn Met Arg Asp Gln Phe Phe Thr Thr Ser Ser
        35                  40                  45

Phe Ala Gly Arg Ile Leu Leu Leu Asp Arg Gly Ile Asn Gly Phe Glu
    50                  55                  60

Val Gln Lys Gln Asn Cys Cys Trp Leu Leu Val Thr His Lys Leu Cys
65                  70                  75                  80

Val Lys Asp Asp Val Ile Val Ala Leu Lys Lys Ala Asn Gly Asp Ala
                85                  90                  95

Thr Leu Lys Phe Glu Pro Phe Val Leu His Val Gln Cys Arg Gln Leu
            100                 105                 110

Gln Asp Ala Gln Ile Leu His Ser Met Ala Ile Asp Ser Gly Phe Arg
        115                 120                 125

Asn Ser Gly Ile Thr Val Gly Lys Arg Gly Lys Thr Met Leu Ala Val
    130                 135                 140

Arg Ser Thr His Gly Leu Glu Val Pro Leu Ser His Lys Gly Lys Leu
145                 150                 155                 160

Met Val Thr Glu Glu Tyr Ile Asp Phe Leu Leu Asn Val Ala Asn Gln
                165                 170                 175

Lys Met Glu Glu Asn Lys Lys Arg Ile Glu Arg Phe Tyr Asn Cys Leu
            180                 185                 190

Gln His Ala Leu Glu Arg Glu Thr Met Thr Asn Leu His Pro Lys Ile
        195                 200                 205

Lys Glu Lys Asn Asn Ser Ser Tyr Ile His Lys Lys Lys Arg Asn Pro
```

```
    210                 215                 220
Glu Lys Thr Arg Ala Gln Cys Ile Thr Lys Glu Ser Asp Glu Glu Leu
225                 230                 235                 240
Glu Asn Asp Asp Asp Asp Asp Leu Gly Ile Asn Val Thr Ile Phe Pro
                245                 250                 255
Glu Asp Tyr
```

Table 15 NHR nucleotide sequence (SEQ ID NO:15)

```
acgcgtgcag gtggcgtggc gccagggatt tgaaccgcgc tgacgaagtt tggtgatcca   60
tcttccgagt atcgccggga tttcgaatcg cgatgatcat cccctctcta gaggagctgg  120
actccctcaa gtacagtgac ctgcagaact tagccaagag tctgggtctc cgggccaacc  180
tgagggcaac caagttgtta aaagccttga aaggctacat taaacatgag gcaagaaaag  240
gaaatgagaa tcaggatgaa agtcaaactt ctgcatcctc ttgtgatgag actgagatac  300
agatcagcaa ccaggaagag ctgagagaca gccacttggc catgtcacca aaacaaggag  360
aaggtgcaag actgtccgtg tggaccctga ctcacagaga atcattcaga gataaaaata  420
agtaatccca ctgaattcca gaatcatgaa aagcaggaaa gccaggatct cagagcactg  480
caaaagttcc ttctccacca gacgagcacc aagaagctga gaatgctgtt tcctcaggta  540
acagagattc aaaggtacct tcagaaggaa agaaatctct ctacacagat gagtcatcca  600
aacctggaaa aaataaaaga actgcaatca ctactccaaa ctttaagaag cttcatgaag  660
ctcattttaa ggaaatggag tccattgatc caatatatng aggagaaaaa aagaaacatt  720
ttgaagaaca caattccatg aatgaactga agcagccgcc catcaataag ggaggggtca  780
ggactccagt acctccaaga ggaagactct ctgtggcttc tactcccatc agccaacgac  840
gctcgcaagg ccggtcttgt ggccctgcaa gtcagagtac cttgggtctg aaggggtcac  900
tcaagcgctc tgctatctct gcagctaaaa cgggtgtcag gttttcagct gctactaaag  960
ataatgagca taagcgttca ctgaccaaga ctccagccag aaagtctgca catgtgaccg 1020
tgtctggggg cacccaaaaa ggcgaggctg tgcttgggac acacaaatta aagaccatca 1080
cggggaattc tgctgctgtt attaccccat tcaagttgac aactgaggca acgcagactc 1140
cagtctccaa taagaaacca gtgtttgatc ttaaagcaag tttgtctcgt cccctcaact 1200
atgaaccaca caaaggaaag ctaaaaccat gggggcaatc taaagaaaat aattatctaa 1260
atcaacatgt caacaaatta acttctacaa gaaaacttac aaacaacccc atctccagac 1320
aaaggaagag caacggaaga aacgcgagca agaagaaagg agaagaaagc aaaggttttg 1380
ggaatgcgaa ggggcctcat tttggctgaa gattaataat tttttaacat cttgtaaata 1440
ttcctgtatt ctcaactttt ttccttttgt aaatttttt tttttgctgt catccccact 1500
ttagtcacga gatcttttc tgctaactgt tcatagtctg tgtagtgtcc atgggttctt 1560
catgtgctat gatctctgaa aagacgttat caccttaaag ctcaaattct ttgggatggt 1620
ttttacttaa gtccattaac aattcaggtt tctaacgaga cccatcctaa aattctcttt 1680
ctagtttttt aatgtcacca tcccaaactc ccgtttctgg atttttaatc cccagctccc 1740
cagttccctc ttatcgtact aatattaaca gaactgcagt cttctgctag ccaatagcat 1800
ttacctgatg gcagctagtt atgcaagctt caggagaatt tgaacaataa caagaatagg 1860
gtaagctggg atagaaaggc cacctcttca ctctctatag aatatagtaa cctttatgaa 1920
acggggccat atagtttggt tatgacatca atattttacc taggtgaaat tgtttaggct 1980
tatgtacctt cgttcaaata tcctcatgta attgccatct gtcactcact atattcacaa 2040
```

```
aaataaaact ctacaactca ttctaacatt gcttacttaa aagctacata gccctatcga   2100
aatgcgagga ttaatgcttt aatgctttta gagacagggt ctcactgtgt tgcccaggct   2160
ggtctcaaac tccaccaaat gtacttctta ttcattttat ggaaaagact aggctttgct   2220
tagtatcatg tccatgtttc cttcacctca gtggagcttc tgagttttat actgctcaag   2280
atcgtcataa ataaaatttt ttctcattgt caaaaaaaaa aaaaaaaaaa aaaaaaaaaa   2340
aaaaaaaaaa aa                                                       2352
```

Table 16 NHR polypeptide sequence (SEQ ID NO:16)

```
Met Ile Ile Pro Ser Leu Glu Glu Leu Asp Ser Leu Lys Tyr Ser Asp
1               5                  10                  15

Leu Gln Asn Leu Ala Lys Ser Leu Gly Leu Arg Ala Asn Leu Arg Ala
            20                  25                  30

Thr Lys Leu Leu Lys Ala Leu Lys Gly Tyr Ile Lys His Glu Ala Arg
        35                  40                  45

Lys Gly Asn Glu Asn Gln Asp Glu Ser Gln Thr Ser Ala Ser Ser Cys
    50                  55                  60

Asp Glu Thr Glu Ile Gln Ile Ser Asn Gln Glu Glu Ala Glu Arg Gln
65                  70                  75                  80

Pro Leu Gly His Val Thr Lys Thr Arg Arg Arg Cys Lys Thr Val Arg
                85                  90                  95

Val Asp Pro Asp Ser Gln Gln Asn His Ser Glu Ile Lys Ile Ser Asn
            100                 105                 110

Pro Thr Glu Phe Gln Asn His Glu Lys Gln Glu Ser Gln Asp Leu Arg
        115                 120                 125

Ala Thr Ala Lys Val Pro Ser Pro Pro Asp Glu His Gln Glu Ala Glu
    130                 135                 140

Asn Ala Val Ser Ser Gly Asn Arg Asp Ser Lys Val Pro Ser Glu Gly
145                 150                 155                 160

Lys Lys Ser Leu Tyr Thr Asp Glu Ser Ser Lys Pro Gly Lys Asn Lys
                165                 170                 175

Arg Thr Ala Ile Thr Thr Pro Asn Phe Lys Lys Leu His Glu Ala His
            180                 185                 190

Phe Lys Glu Met Glu Ser Ile Asp Pro Ile Tyr Xaa Gly Glu Lys Lys
        195                 200                 205

Lys His Phe Glu Glu His Asn Ser Met Asn Glu Leu Lys Gln Pro Pro
    210                 215                 220

Ile Asn Lys Gly Gly Val Arg Thr Pro Val Pro Pro Arg Gly Arg Leu
225                 230                 235                 240

Ser Val Ala Ser Thr Pro Ile Ser Gln Arg Arg Ser Gln Gly Arg Ser
                245                 250                 255

Cys Gly Pro Ala Ser Gln Ser Thr Leu Gly Leu Lys Gly Ser Leu Lys
            260                 265                 270

Arg Ser Ala Ile Ser Ala Ala Lys Thr Gly Val Arg Phe Ser Ala Ala
```

```
        275                 280                 285
Thr Lys Asp Asn Glu His Lys Arg Ser Leu Thr Lys Thr Pro Ala Arg
    290                 295                 300
Lys Ser Ala His Val Thr Val Ser Gly Gly Thr Gln Lys Gly Glu Ala
305                 310                 315                 320
Val Leu Gly Thr His Lys Leu Lys Thr Ile Thr Gly Asn Ser Ala Ala
                325                 330                 335
Val Ile Thr Pro Phe Lys Leu Thr Thr Glu Ala Thr Gln Thr Pro Val
            340                 345                 350
Ser Asn Lys Lys Pro Val Phe Asp Leu Lys Ala Ser Leu Ser Arg Pro
        355                 360                 365
Leu Asn Tyr Glu Pro His Lys Gly Lys Leu Lys Pro Trp Gly Gln Ser
    370                 375                 380
Lys Glu Asn Asn Tyr Leu Asn Gln His Val Asn Arg Ile Asn Phe Tyr
385                 390                 395                 400
Lys Lys Thr Tyr Lys Gln Pro His Leu Gln Thr Lys Glu Glu Gln Arg
                405                 410                 415
Lys Lys Arg Glu Gln Glu Arg Lys Glu Lys Lys Ala Lys Val Leu Gly
            420                 425                 430
Met Arg Arg Gly Leu Ile Leu Ala Glu Asp
        435                 440
```

Table 17 displays alignment of hMX1, hMX2 with human myosin (SEQ ID NO:31; GenBank AF247457) (Berg *et al.*, 2000). As seen from the alignment, hMX1 and hMX2 have a likely N-terminus of M N D residues. One of skill in the art can easily verify this observation by probing cDNA or genomic human libraries, or PCR techniques, to acquire the full length polynucleotide sequence.

Table 17 Alignment of hMX1, hMX2 and human myosin X

```
10          1 ---FCLQGTRVWLRENGQHFPSTVNSCAEGIVVFRTDYGQVFTYKQSTIT
12          1 ---FCLQGTRVWLRENGQHFPSTVNSCAEGIVVFRTDYGQVFTYKQSTIT
humX        1 MDNFFTEGTRVWLRENGQHFPSTVNSCAEGIVVFRTDYGQVFTYKQSTIT

10         48 HQKVTAMHPTNEEGVDDMASLTELHGGSIMYNLFQRYKRNQIWTYIGSIL
12         48 HQKVTAMHPTNEEGVDDMASLTELHGGSIMYNLFQRYKRNQIWTYIGSIL
humX       51 HQKVTAMHPTNEEGVDDMASLTELHGGSIMYNLFQRYKRNQIYTYIGSIL

10         98 ASVNPYQPIAGLYEPATMEQYSRRHLGELPPHIFAIANECYRCLWKRHDN
12         98 ASVNPYQPIAGLYEPATMEQYSRRHLGELPPHIFAIANECYRCLWKRHDN
humX      101 ASVNPYQPIAGLYEPATMEQYSRRHLGELPPHIFAIANECYRCLWKRYDN

10        148 QCILIKGESGAGKTESTKLILKFLSVISQQSLELSLKEKTSCVERAILES
12        148 QCILIKGESGAGKTESTKLILKFLSVISQQSLELSLKEKTSCVERAILES
humX      151 QCILISGESGAGKTESTKLILKFLSVISQQSLELSLKEKTSCVERAILES

10        198 SPIMEAFGNAKTVYNNNSSRFGKFVQLNICQKGNIQGGRIVDCILSSQNR
```

```
12      198 SPIMEAFGNAKTVYNNNSSRFGKFVQLNICQKGNIQGGRIVDCILSSQNR
humX    201 SPIMEAFGNAKTVYNNNSSRFGKFVQLNICQKGNIQGGRIVDYLLE-KNR

10      248 VVRQNPGERNYHIFYALLAGLEHEEREEFYLSTPENYHYLNQSGCVEDKT
12      248 VVRQNPGERNYHIFYALLAGLEHEEREEFYLSTPENYHYLNQSGCVEDKT
humX    250 VVRQNPGERNYHIFYALLAGLEHEEREEFYLSTPENYHYLNQSGCVEDKT

10      298 ISDQESFREVITAMDVMQFSKEEVREVSRLLAGILHLGNIEFITAGGAQV
12      298 ISDQESFREVITAMDVMQFSKEEVREVSRLLAGILHLGNIEFITAGGAQV
humX    300 ISDQESFREVITAMDVMQFSKEEVREVSRLLAGILHLGNIEFITAGGAQV

10      348 SFKTALGRSAELLGLDPTQLTDALTQRSMFLRGEEILTPLNVQQAVDSRD
12      348 SFKTALGRSAELLGLDPTQLTDALTQRSMFLRGEEILTPLNVQQAVDSRD
humX    350 SFKTALGRSAELLGLDPTQLTDALTQRSMFLRGEEILTPLNVQQAVDSRD

10      398 SLAMALYACCFEWVIKKINSRIKGNEDFKSIGILDIFGFENFEVNHFEQF
12      398 SLAMALYACCFEWVIKKINSRIKGNEDFKSIGILDIFGFENFEVNHFEQF
humX    400 SLAMALYACCFEWVIKKINSRIKGNEDFKSIGILDIFGFENFEVNHFEQF

10      448 NINYANEKLQEYFNKHIFSLEQLEYSREGLVWEDIDWIDNGECLDLIEKK
12      448 NINYANEKLQEYFNKHIFSLEQLEYSREGLVWEDIDWIDNGECLDLIEKK
humX    450 NINYANEKLQEYFNKHIFSLEQLEYSREGLVWEDIDWIDNGECLDLIEKK

10      498 LGLLLALINEESHFPQATDSTLLEKLHSQHANNHFYVKPRVAVNNFGVKHY
12      498 LGLLLALINEESHFPQATDSTLLEKLHSQHANNHFYVKPRVAVNNFGVKHY
humX    500 LGLLLALINEESHFPQATDSTLLEKLHSQHANNHFYVKPRVAVNNFGVKHY

10      548 AGEVQYDVRGILEKNRDTFRDDLLNLLRESRFDFIYDLFEHVSSRNNQDT
12      548 AGEVQYDVRGILEKNRDTFRDDLLNLLRESRFDFIYDLFEHVSSRNNQDT
humX    550 AGEVQYDVRGILEKNRDTFRDDLLNLLRESRFDFIYDLFEHVSSRNNQDT

10      598 LKCGSKHRRPTVSSQFKVDSLHSLMATLSSSNPFFVRCIKPNMQKMPDQF
12      598 LKCGSKHRRPTVSSQFKVDSLHSLMATLSSSNPFFVRCIKPNMQKMPDQF
humX    600 LKCGSKHRRPTVSSQFKDS-LHSLMATLSSSNPFFVRCIKPNMQKMPDQF

10      648 DQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPED
12      648 DQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPED
humX    649 DQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYKVLMRNLALPED

10      698 VRGKCTSLLQLYDASNSEWQLGKTKVFLRESLEQKLEKRREEEVSHAAMV
12      698 VRGKCTSLLQLYDASNSEWQLGKTKVFLRESLEQKLEKRREEEVSHAAMV
humX    699 VRGKCTSLLQLYDASNSEWQLGKTKVFLRESLEQKLEKRREEEVSHAAMV

10      748 IRAHVLGFLARKQYRKVLYCVVIIQKNYRAFLLRRRFLHLKKAAIVFQKQ
12      748 IRAHVLGFLARKQYRKVLYCVVIIQKNYRAFLLRRRFLHLKKAAIVFQKQ
humX    749 IRAHVLGFLARKQYRKVLYCVVIIQKNYRAFLLRRRFLHLKKAAIVFQKQ

10      798 LRGQIARRVYRQLLAEKREQEEKKKQEEEEKKKREEEERERERERRREAEL
12      798 LRGQIARRVYRQLLAEKREQEEKKKQEEEEKKKREEEERERERERRREAEL
humX    799 LRGQIARRVYRQLLAEKREQEEKKKQEEEEKKKREEEERERERERRREAEL

10      848 RAQQEEETRKQQELEALQKSQKEAELTRELEKQKENKQVEEILRLEKEIE
12      848 RAQQEEETRKQQELEALQKSQKEAELTRELEKQKENKQVEEILRLEKEIE
humX    849 RAQQEEETRKQQELEALQKSQKEAELTRELEKQKENKQVEEILRLEKEIE

10      898 DLQRMKEQQELSLTEASLQKLQERRDQELRRLEEEACRAAQEFLESLNFD
12      898 DLQRMKEQQELSLTEASLQKLQERRDQELRRLEEEACRAAQEFLESLNFD
humX    899 DLQRMKEQQELSLTEASLQKLQERRDQELRRLEEEACRAAQEFLESLNFD

10      948 EIDECVRNIERSLSGGSEFSSELAESACEEKPNFNFSQPYPEEEVDEGFE
12      948 EIDECVRNIERSLSGGSEFSSELAESACEEKPNFNFSQPYPEEEVDEGFE
humX    949 EIDECVRNIERSLSVGSEFSSELAESACEEKPNFNFSQPYPEEEVDEGFE

10      998 ADDDAFKDSPNPSEHGHSDQRTSGIRTSDDSSEEDPYMNDTVVPTSPSAD
12      998 ADDDAFKDSPNPSEHGHSDQRTSGIRTSDDSSEEDPYMNDTVVPTSPSAD
humX    999 ADDDAFKDSPNPSEHGHSDQRTSGIRTSDDSSEEDPYMNDTVVPTSPSAD
```

```
10      1048 STVLLAPSVQDSGSLHNSSSGESTYCMPQNAGDLPSPDGDYDYDQDDYED
12      1048 STVLLAPSVQDSGSLHNSSSGESTYCMPQNAGDLPSPDGDYDYDQDDYED
humX    1049 STVLLAPSVQDSGSLHNSSSGESTYCMPQNAGDLPSPDGDYDYDQDDYED

10      1098 GAITSGSSVTFSNSYGSQWSPDYRCSVGTYNSSGAYRFSSEGAQSSFEDS
12      1098 GAITSGSSVTFSNSYGSQWSPDYRCSVGTYNSSGAYRFSSEGAQSSFEDS
humX    1099 GAITSGSSVTFSNSYGSQWSPDYRCSVGTYNSSGAYRFSSEGAQSSFEDS

10      1148 EEDFDSRFDTDDELSYRRDSVYSCVTLPYFHSFLYMKGGLMNSWKRRWCV
12      1148 EEDFDSRFDTDDELSYRRDSVYSCVTLPYFHSFLYMKGGLMNSWKRRWCV
humX    1149 EEDFDSRFDTDDELSYRRDSVYSCVTLPYFHSFLYMKGGLMNSWKRRWCV

10      1198 LKDETFLWFRSKQEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMY
12      1198 LKDETFLWFRSKQEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMY
humX    1199 LKDETFLWFRSKQEALKQGWLHKKGGGSSTLSRRNWKKRWFVLRQSKLMY

10      1248 FENDSEEKLKGTVEVRTAKEIIDNTTKENGIDIIMADRTFHLIAESPEDA
12      1248 FENDSEEKLKGTVEVRTAKEIIDNTTKENGIDIIMADRTFHLIAESPEDA
humX    1249 FENDSEEKLKGTVEVRTAKEIIDNTTKENGIDIIMADRTFHLIAESPEDA

10      1298 SQWFSVLSQVHASTDQEIQEMHDEQANPQNAVGTLDVGLIDSVCASDSPD
12      1298 SQWFSVLSQVHASTDQEIQEMHDEQANPQNAVGTLDVGLIDSVCASDSPD
humX    1299 SQWFSVLSQVHASTDQEIQEMHDEQANPQNAVGTLDVGLIDSVCASDSPD

10      1348 RPNSFVIITANRVLHCNADTPEEMHHWITLLQRSKGDTRVEGQEFIVRGW
12      1348 RPNSFVIITANRVLHCNADTPEEMHHWITLLQRSKGDTRVEGQEFIVRGW
humX    1349 RPNSFVIITANRVLHCNADTPEEMHHWITLLQRSKGDTRVEGQEFIVRGW

10      1398 LHKEVKNSPKMSSLKLKKRWFVLTHNSLDYYKSSEKNALKLGTLVLNSLC
12      1398 LHKEVKNSPKMSSLKLKKRWFVLTHNSLDYYKSSEKNALKLGTLVLNSLC
humX    1399 LHKEVKNSPKMSSLKLKKRWFVLTHNSLDYYKSSEKNALKLGTLVLNSLC

10      1448 SVVPPDEKIFKETGYWNVTVYGRKHCYRLYTKLLNEATRWSSVIQNVTDT
12      1448 SVVPPDEKIFKETGYWNVTVYGRKHCYRLYTKLLNEATRWSSVIQNVTDT
humX    1449 SVVPPDEKIFKETGYWNVTVYGRKHCYRLYTKLLNEATRWSSAIQNVTDT

10      1498 KAPIDTPTQQLIQDIKENCLNSDVVEQIYKRNPILRYTHHPLHSPLLPLP
12      1498 KAPIDTPTQQLIQDIKENCLNSDVVEQIYKRNPILRYTHHPLHSPLLPLP
humX    1499 KAPIDTPTQQLIQDIKENCLNSDVVEQIYKRNPILRYTHHPLHSPLLPLP

10      1548 YGDINLNLLKDKGYTTLQDEAIKIFNSLQQLESMSDPIPIIQGILQTGHD
12      1548 YGDINLNLLKDKGYTTLQDEAIKIFNSLQQLESMSDPIPIIQGILQTGHD
humX    1549 YGDINLNLLKDKGYTTLQDEAIKIFNSLQQLESMSDPIPIIQGILQTGHD

10      1598 LRPLRDELYCQLIKQTNKVPHPGSVGNLYSWQILTCLSCTFLPSRGILKY
12      1598 LRPLRDELYCQLIKQTNKVPHPGSVGNLYSWQILTCLSCTFLPSRGILKY
humX    1599 LRPLRDELYCQLIKQTNKVPHPGSVGNLYSWQILTCLSCTFLPSRGILKY

10      1648 LKFHLKRIREQFPGTEMEKYALFTYESLKKTKCREFVPSRDEIEALIHRQ
12      1648 LKFHLKRIREQFPGTEMEKYALFTYESLKKTKCREFVPSRDEIEALIHRQ
humX    1649 LKFHLKRIREQFPGTEMEKYALFTYESLKKTKCREFVPSRDEIEALIHRQ

10      1698 EMTSTVYCHGGGSCKITINSHTTAGEVVEKLIRGLAMEDSRNMFALFEYN
12      1698 EMTSTVYCHGGGSCKITINSHTTAGEVVEKLIRGLAMEDSRNMFALFEYN
humX    1699 EMTSTVYCHGGGSCKITINSHTTAGEVVEKLIRGLAMEDSRNMFALFEYN

10      1748 GHVDKAIESRTVVADVLAKFEKLAATSEVGDLPWKFYFKLYCFLDTDNVP
12      1748 GHVDKAIESRTVVADVLAKFEKLAATSEVGDLPWKFYFKLYCFLDTDNVP
humX    1749 GHVDKAIESRTVVADVLAKFEKLAATSEVGDLPWKFYFKLYCFLDTDNVP

10      1798 KDSVEFAFMFEQAHEAVIHGHHPAPEENLQVLAALRLQYLQGDYTLHAAI
12      1798 KDSVEFAFMFEQAHEAVIHGHHPAPEENLQVLAALRLQYLQGDYTLHAAI
humX    1799 KDSVEFAFMFEQAHEAVIHGHHPAPEENLQVLAALRLQYLQGDYTLHAAI

10      1848 PPLEEVYSLQRLKARISQSTKTFTPCERLEKRRTSFLEGTLRRSFRTGSV
```

```
12      1848 PPLEEVYSLQRLKARISQSTKTFTPCERLEKRRTSFLEGTLRRSFRTGSV
humX    1849 PPLEEVYSLQRLKARISQSTKTFTPCERLEKRRTSFLEGTLRRSFRTGSV

10      1898 VRQKVEEEQMLDMWIKEEVSSARASIIDKWRKFQGMNQEQAMAKYMALIK
12      1898 VRQKVEEEQMLDMWIKEEVSSARASIIDKWRKFQGMNQEQAMAKYMALIK
humX    1899 VRQKVEEEQMLDMWIKEEVSSARASIIDKWRKFQGMNQEQAMAKYMALIK

10      1948 EWPGYGSTLFDVECKEGGFPQELWLGVSADAVSVYKRGEGRPLEVFQYEH
12      1948 EWPGYGSTLFDVEVRTG-CHVLGWAGCWHLRTWITAKFMWREDKMEHFAL
humX    1949 EWPGYGSTLFDVECKEGGFPQELWLGVSADAVSVYKRGEGRPLEVFQYEH

10      1998 ILSFGAPLANTYKIVVDERELLFETSEVVDVAKLMKAYISMIVKKRYSTT
12      1997 STSFFRAPKIVPLTPPFSSQFLFSCVVNASVILGMNAKLRCHLFFYPSLG
humX    1999 ILSFGAPLANTYKIVVDERELLFETSEVVDVAKLMKAYISMIVKKRYSTT

10      2048 RSASSQGSSR
12      2047 KL--------
humX    2049 RSASSQGSSR
```

The invention also includes polypeptides and nucleotides having 80-100%, including 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 and 99%, sequence identity to SEQ ID NOS:1-16, as well as nucleotides encoding any of these polypeptides, and compliments of any of these nucleotides. In an alternative embodiment, polypeptides and/or nucleotides (and compliments thereof) identical to any one of, or more than one of, SEQ ID NOS:1-16 are excluded. In yet another embodiment, polypeptides and/or nucleotides (and compliments thereof) having 81-100% identical, including 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 and 99%, sequence identity to SEQ ID NOS:1-16 are excluded.

The nucleic acids and proteins of the invention are potentially useful in promoting wound healing, for example after organ transplantation, or in the treatment of myocardial infarction, but also in treating tumors, and in cancers, diabetic retinopathy, macular degeneration, psoriasis, and rheumatoid arthritis. For example, a cDNA encoding AAP may be useful in gene therapy, and AAP proteins may be useful when administered to a subject in need thereof. The novel nucleic acid encoding AAP, and the AAP proteins of the invention, or fragments thereof, may further be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein are to be assessed. These materials are further useful in the generation of Abs.that bind immunospecifically to the novel substances of the invention for use in therapeutic or diagnostic methods.

Kelch-like protein (KLP)

The putative protein encoded by *KLP* contains 1 putative BTB domain and 4 putative Kelch motifs. The BTB (broad complex, tramtrack, bric-a-brac)/POZ (poxvirus, zinc finger) domain is involved in protein protein interactions. The kelch motif is sixfold tandem element in the sequence of the *Drosophila* kelch ORF1 protein that also contains BTB. Kelch ORF1 localizes to the ring canals in the egg chamber and helps to organize the F-actin cytoskeleton (Adams *et al.*, 2000). The repeated kelch motifs predict a conserved tertiary structure, a β-propeller. This module appears in many different polypeptide contexts and contains multiple potential protein-protein interaction sites. Members of this growing superfamily are present throughout the cell and extracellularly and have diverse activities (Adams *et al.*, 2000). Such activities include cytoskeleton organization, as well as other morphological processes, gene expression, interactions with viruses, and various extracellular events, such as cell spreading.

Alignment with *Drosophila* kelch and other kelch-like proteins, human kelch-like protein (GenBank AAF20938 (SEQ ID NO:17)), hypothetical *C. elegans* (GenBank O61795 (SEQ ID NO:18) and the skeletal muscle-specific sarcosin (GenBank O60662 (SEQ ID NO:19); (Taylor *et al.*, 1998)) reveals that the disclosed protein (SEQ ID NO:2) is a member of a new subfamily

KLP is associated with tube formation and angiogenesis because it is upregulated in the *in vitro* model of angiogenesis of Example 1. Kelch mediates cytoskeletal associations, it is involved in morphogenetic processes, such as tube formation, that depend on cytoskeletal arrangements and signaling. KLP represents an attractive target for small molecule drug therapy.

Human ortholog of mouse BAZF (hBAZF)

hBAZF (SEQ ID NO:4) is the human ortholog of mouse BAZF (GenBank AB011665; SEQ ID NO:20), BAZF is a Bcl-6 (LAZ3) homolog, a transcription repressor that controls germinal center formation and the T cell-dependent immune response. Expression of Bcl-6 negatively correlates with cellular proliferation: Bcl-6 suppresses growth associated with impaired mitotic S phase progression and apoptosis (Albagli *et al.*, 1999).

BAZF contains a BTB/POZ domain and five repeats of the Kruppel-like zinc finger motifs, instead of 6 in Bcl-6 (Okabe *et al.*, 1998). Expression of *BAZF* mRNA is

relegated to heart and lung, unlike *Bcl-6* mRNA, but is induced in activated lymphocytes as an immediate-early gene, like *Bcl-6* (Okabe *et al.*, 1998).

The hBAZF sequence was derived by using tblastn (protein query –translated database) (Altschul *et al.*, 1997), with the mouse protein sequence (GenBank O88282; SEQ ID NO:21) that has homology to GenBank AC015918 (SEQ ID NO:22), a clone of *Homo sapiens* chromosome 17. Human BAZF contains five Kruppel-like zinc finger motif repeats and a BTB/POZ domain.

The peptide sequence, "RSQ...PQV" that is present in the human sequence, might represent an alternative spliced form of the gene. Aligment with mouse BAZF, and aligment with mouse and human Bcl-6 demonstrates that the four proteins are almost identical in this region, but only human BAZF has this inserted sequence.

hBAZF is upregulated in HUVE cells grown embedded in collagen gels but not as a monolayer grown on collagen. When HUVE cells are suspended in collagen, they do not proliferate. Analagous to the role of mBAZF plays a role in regulating cell proliferation (Okabe *et al.*, 1998), hBAZF plays a roll in cell proliferation in HUVE suspended in collagen. Because of its high expression during vessel morphogenesis, hBAZF represents an excellent molecular marker, as well as an attractive target for various therapies to inhibit angiogenesis.

hmt-Elongation Factor G (hEF-G)

The original isolation of hEF-G (SEQ ID NO:6) is 84% identical and colinear with *Rattus norvegicus* nuclear encoded mitochondrial elongation factor G (GenBank L14684 (SEQ ID NO:23); (Barker *et al.*, 1993). No human gene is described in GenBank. However, searching EST databases, the human gene is contained inside GenBank AC010936 (SEQ ID NO:24), a chromosome 3 clone. Aligment of hEF-G with rat mtEF-G and yeast EF-G1 demonstrates that the novel sequence is the ortholog of rat nuclear-encoded mitochondrial elongation factor G.

Bacterial elongation factor G (EF-G) physically associates with translocation-competent ribosomes and facilitates transition to the subsequent codon through the coordinate binding and hydrolysis of GTP. The deduced amino acid sequence of hmt-EF-G reveals characteristic motifs shared by all GTP binding proteins. Therefore, similarly

to other elongation factors, the enzymatic function of hmt-EF-G is predicted to depend on GTP binding and hydrolysis.

Hmt-EF-G is strongly induced (30-fold) in an *in vitro* model of angiogenesis (Example 1), and as such, hmt-EF-G represents an excellent molecular marker for vessel formation. Because of its putative localization to the mitochondrion, hmt-EF-G is also an attractive therapeutic target to treat disease states associated with mitochondrial dysfunction.

Human thyroid regulated transcript (hTRG)

hTRG (SEQ ID NO:8) is the human ortholog of rat TRG, a novel thyroid transcript negatively regulated by TSH (GenBank KIAA1058 (SEQ ID NO:25); (Bonapace *et al.*, 1990).

SEQ ID NO:25 appears to be a partial peptide since there are *C. elegans* homologous proteins of 2000 residues. Using tblastn (Altschul *et al.*, 1997) against genomic sequences, the hTRG sequence (SEQ ID NO:8) was assembled.

In *C. elegans*, homologous proteins localize either to the plasma membrane or to the mitochondrial inner membrane. A partial sequence, KIAA0694 (SEQ ID NO:26) also localizes to the mitochondrial matrix. hTRG has a PH domain, and has weak homology to an extracellular fibronectin-binding protein precursor. SEQ ID NO:26 has homology to *Drosophila* DOS and mouse Gab-2 proteins; both of which are involved in signal transduction, acting as adapter proteins between receptors and kinases like Ras1 (Hibi and Hirano, 2000).

Because of hTRG is upregulated during the *in vitro* model of angiogenesis (Example 1), and because of its homologies with adapter proteins, hTRG is likely to be involved in signal transduction between receptors and kinases. As such, hTRG represent an excellent candidate for small molecule drug therapy to modulate angiogenesis and treat angiogenesis-related diseases. In addition, because of its putative ability to respond to thyroid stimulating hormone (TSH), modulation of hTRG is useful to treat diseases related to TSH imbalance.

Human myosin X (hMX1(SEQ ID NO:10) and hMX2 (SEQ ID NO:12)

The hMX proteins represent the human ortholog of bovine myosin X, (GenBank AAB39486; SEQ ID NO:27). Using tblastn (Altschul *et al.*, 1997) and the bovine sequence, a series of genomic clones from human chromosome 5 were identified; GenBank AC010310 (SEQ ID NO:28) appears to contain the entire sequence. Interestingly, a partial cDNA sequence from mouse (GenBank AF184153; SEQ ID NO:29) localizes to a 0.8 cM interval on the short arm of chromosome 5, between the polymorphic microsatellite markers D5S416 and D5S2114. In this region lies the gene for familial chondrocalcinosis (*CCAL2*) (Rojas *et al.*, 1999).

Another GenBank entry, AB018342 (SEQ ID NO:30) that represents the 3' region of *hMX*, appears to encode an alternative splice form. Noteworthy, this variant (hMX2) has a very hydrophobic carboxy terminus, while the more prevalent form (hMX1) is hydrophilic and potentially interacts with DNA/RNA since it has homology to high mobility group box (HMG) and ribosomal proteins. Additionaly, a myosin head domain was found in the NH terminus, as well as a myosin talin domain, two calmodulin binding domains, four pleckstrin domains and a band 4.1 domain.

The band 4.1 domain represents a crossroads between cytoskeletal organization and signal transduction. The domain was first described in the red blood cell protein band 4.1. The ERM proteins ezrin, radixin, and moesin and the unconventional myosins VIIa and X all possess the band 4.1 domain (Louvet-Vallee, 2000). The band 4.1 domain binds single transmembrane protein at the membrane-proximal region in the C-terminal cytoplasmic tail.

HMX is upregulated during angiogenesis in an *in vitro* model (Example 1). Because hMX contains the protein-protein interaction domains PH and band 4.1 domain, hMX1 and hMX2 are involved in angiogenesis, likely transducing signals from angiogenic factors, perhaps modulating the cytoskeleton.

Human mitochondrial protein (hMP)

Analysis of hMP (SEQ ID NO:14) reveals several subdomain that are homologous to proteins involved in transport across membranes, K^+ATPase α and γ chains. Further analysis indicates that hMP may bind DNA and or RNA, since hMP is homologous to histones and transcription factors, especially those possessing basic region plus leucine zipper domains.

Although PSORT analysis (Nakai and Horton, 1999) predicts nuclear localization (P=.6), hMP may in fact be a nuclear-encoded mitochondrial protein. Homologies with mostly bacterial proteins and a PSORT prediction ofmitochondrial matrix space localization (P=0.4478) strongly support this contention.

Because hMP is upregulated in an *in vitro* model of angiogenesis (Example 1), and because of its homologies with mitochondrial and nuclear-localized polypeptides, hMP is important in vascular morphogenesis, most likely through either powering the cellular differentiation-redifferentiation process, and/or affecting changes in the nuclear matrix that change global gene expression. Alternatively, hMP may be a transcription factor for either the nuclear or mitochondrial genomes.

Nuclear hormone receptor (NHR)

NHR (SEQ ID NO:16) has two domains: (1) the NH region is similar to Swi3 (yeast SWI/SNF complexes regulate transcription by chromatin remodeling), indicating a role in transcriptional regulation, and (2) the COOH region is similar to parathyroid hormone-related proteins that bind parathyroid hormones. PSORT (Nakai and Horton, 1999) predicts the protein to localize in the nucleus P=0.9600.

The identification of this new putative hormone receptor-transcriptional regulator and hBAZF suggest a novel human transcriptional pathway that resembles, to some extent, that of Bcl-6.

Bcl-6 suppresses transcription via the BTB domain, which recruits a complex containing SMRT, retinoid thyroid hormone receptor, nuclear receptor corepressor (N-CoR), mammalian Sin3A, and histone deacetylase (HDAC). hBAZF, which also possesses a BTB domain, might recruit a similar complex containing deacetylase. Expression data indicate that *hBAZF* is up-regulated while *NHR* is down-regulated. These data agree with other evidence related to tube formation. Testosterone (a steroid) and dexamethasone (a steroid-like molecule) strongly inhibit vessel formation, and all-trans retinoic acid (at-RA) and 9-cis retinoic acid (9-cis RA) stimulate capillary-like tubular structures (Lansink *et al.*, 1998).

Upon angiogenic stimulation, endothelial cells may become incompetent to respond to anti-angiogenic responses mediated by hormones using a dual mechanism, sequestering hormones and suppressing transcription. Because nHR is down-regulated

during *in vitro* angiogenesis (Example 1), this polypeptide is likely to be involved in non-angiogenesis-specific gene transcription. nHR is an attractive therapeutic target, especially in therapies that are directed at preventing vascularization.

AAP *polynucleotides*

One aspect of the invention pertains to isolated nucleic acid molecules that encode AAP or biologically-active portions thereof. Also included in the invention are nucleic acid fragments sufficient for use as hybridization probes to identify AAP-encoding nucleic acids (*e.g.*, *AAP* mRNAs) and fragments for use as polymerase chain reaction (PCR) primers for the amplification and/or mutation of *AAP* molecules. A "nucleic acid molecule" includes DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs. The nucleic acid molecule may be single-stranded or double-stranded, but preferably comprises double-stranded DNA.

1. *probes*

Probes are nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or many (*e.g.*, 6,000 nt) depending on the specific use. Probes are used to detect identical, similar, or complementary nucleic acid sequences. Longer length probes can be obtained from a natural or recombinant source, are highly specific, and much slower to hybridize than shorter-length oligomer probes. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies. Probes are substantially purified oligonucleotides that will hybridize under stringent conditions to at least optimally 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 consecutive sense strand nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, or 15; or an anti-sense strand nucleotide sequence of these sequences; or of a naturally occurring mutant of these sequences.

The full- or partial length native sequence *AAP* may be used to "pull out" similar (homologous) sequences (Ausubel *et al.*, 1987; Sambrook, 1989), such as: (1) full-length or fragments of AAP cDNA from a cDNA library from any species (*e.g.* human, murine, feline, canine, bacterial, viral, retroviral, yeast), (2) from cells or tissues, (3) variants within a species, and (4) homologues and variants from other species. To find related sequences that may encode related genes, the probe may be designed to encode unique

sequences or degenerate sequences. Sequences may also be genomic sequences including promoters, enhancer elements and introns of native sequence *AAP*.

For example, an *AAP* coding region in another species may be isolated using such probes. A probe of about 40 bases is designed, based on an *AAP*, and made. To detect hybridizations, probes are labeled using, for example, radionuclides such as ^{32}P or ^{35}S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin-biotin systems. Labeled probes are used to detect nucleic acids having a complementary sequence to that of an *AAP* in libraries of cDNA, genomic DNA or mRNA of a desired species.

Such probes can be used as a part of a diagnostic test kit for identifying cells or tissues which mis-express an AAP, such as by measuring a level of an *AAP* in a sample of cells from a subject *e.g.*, detecting *AAP* mRNA levels or determining whether a genomic *AAP* has been mutated or deleted.

2. *isolated nucleic acid*

An isolated nucleic acid molecule is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Preferably, an isolated nucleic acid is free of sequences that naturally flank the nucleic acid (*i.e.*, sequences located at the 5'- and 3'-termini of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, isolated *AAP* molecules can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell/tissue from which the nucleic acid is derived (*e.g.*, brain, heart, liver, spleen, *etc.*). Moreover, an isolated nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement of this aforementioned nucleotide sequence, can be isolated using standard molecular biology techniques and the provided sequence information. Using all or a portion of the nucleic acid sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 as a hybridization probe, *AAP*

molecules can be isolated using standard hybridization and cloning techniques (Ausubel *et al.*, 1987; Sambrook, 1989).

PCR amplification techniques can be used to amplify *AAP* using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers. Such nucleic acids can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to *AAP* sequences can be prepared by standard synthetic techniques, *e.g.*, an automated DNA synthesizer.

3. *oligonucleotide*

An oligonucleotide comprises a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction or other application. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment of the invention, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, or a complement thereof. Oligonucleotides may be chemically synthesized and may also be used as probes.

4. *complementary nucleic acid sequences; binding*

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 or 15, or a portion of this nucleotide sequence (*e.g.*, a fragment that can be used as a probe or primer or a fragment encoding a biologically-active portion of an AAP). A nucleic acid molecule that is complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, is one that is sufficiently complementary to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, thereby forming a stable duplex.

"Complementary" refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term "binding" means the physical

or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, van der Waals, hydrophobic interactions, and the like. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

Nucleic acid fragments are at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full-length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice.

5. *derivatives, and analogs*

Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differ from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type. Homologs are nucleic acid sequences or amino acid sequences of a particular gene that are derived from different species.

Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the invention, in various embodiments, by at least about 70%, 80%, or 95% identity (with a preferred identity of 80-95%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the

aforementioned proteins under stringent, moderately stringent, or low stringent conditions (Ausubel *et al.*, 1987).

6. *homology*

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of AAP. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, different genes can encode isoforms. In the invention, homologous nucleotide sequences include nucleotide sequences encoding for an AAP of species other than humans, including, but not limited to: vertebrates, and thus can include, *e.g.*, frog, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the exact nucleotide sequence encoding human AAP. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, as well as a polypeptide possessing AAP biological activity. Various biological activities of the AAP are described below.

7. *open reading frames*

The open reading frame (ORF) of an *AAP* gene encodes an AAP. An ORF is a nucleotide sequence that has a start codon (ATG) and terminates with one of the three "stop" codons (TAA, TAG, or TGA). In this invention, however, an ORF may be any part of a coding sequence that may or may not comprise a start codon and a stop codon. To achieve a unique sequence, preferable *AAP* ORFs encode at least 50 amino acids.

AAP polypeptides

1. *mature*

An *AAP* can encode a mature AAP. A "mature" form of a polypeptide or protein disclosed in the present invention is the product of a naturally occurring polypeptide or precursor form or proprotein. The naturally occurring polypeptide, precursor or proprotein includes, by way of nonlimiting example, the full-length gene product,

encoded by the corresponding gene. Alternatively, it may be defined as the polypeptide, precursor or proprotein encoded by an open reading frame described herein. The product "mature" form arises, again by way of nonlimiting example, as a result of one or more naturally occurring processing steps as they may take place within the cell, or host cell, in which the gene product arises. Examples of such processing steps leading to a "mature" form of a polypeptide or protein include the cleavage of the N-terminal methionine residue encoded by the initiation codon of an open reading frame, or the proteolytic cleavage of a signal peptide or leader sequence. Thus a mature form arising from a precursor polypeptide or protein that has residues 1 to N, where residue 1 is the N-terminal methionine, would have residues 2 through N remaining after removal of the N-terminal methionine. Alternatively, a mature form arising from a precursor polypeptide or protein having residues 1 to N, in which an N-terminal signal sequence from residue 1 to residue M is cleaved, would have the residues from residue M+1 to residue N remaining. Further as used herein, a "mature" form of a polypeptide or protein may arise from a step of post-translational modification other than a proteolytic cleavage event. Such additional processes include, by way of non-limiting example, glycosylation, myristoylation or phosphorylation. In general, a mature polypeptide or protein may result from the operation of only one of these processes, or a combination of any of them.

2. *active*

An active AAP polypeptide or AAP polypeptide fragment retains a biological and/or an immunological activity similar, but not necessarily identical, to an activity of a naturally-occuring (wild-type) AAP polypeptide of the invention, including mature forms. A particular biological assay, with or without dose dependency, can be used to determine AAP activity. A nucleic acid fragment encoding a biologically-active portion of AAP can be prepared by isolating a portion of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 that encodes a polypeptide having an AAP biological activity (the biological activities of the AAP are described below), expressing the encoded portion of AAP (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of AAP. Immunological activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native AAP; biological activity refers to a function, either inhibitory or stimulatory, caused by a native AAP that excludes immunological activity.

AAP *nucleic acid variants and hybridization*

1. *variant polynucleotides, genes and recombinant genes* The invention further encompasses nucleic acid molecules that differ from the nucleotide sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 due to degeneracy of the genetic code and thus encode the same AAP as that encoded by the nucleotide sequences shown in SEQ ID NO NOS:1, 3, 5, 7, 9, 11, 13 or 15. An isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16.

In addition to the *AAP* sequences shown in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, DNA sequence polymorphisms that change the amino acid sequences of the AAP may exist within a population. For example, allelic variation among individuals will exhibit genetic polymorphism in an *AAP*. The terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame (ORF) encoding an AAP, preferably a vertebrate AAP. Such natural allelic variations can typically result in 1-5% variance in an *AAP*. Any and all such nucleotide variations and resulting amino acid polymorphisms in an AAP, which are the result of natural allelic variation and that do not alter the functional activity of an AAP are within the scope of the invention.

Moreover, *AAP* from other species that have a nucleotide sequence that differs from the human sequence of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15, are contemplated. Nucleic acid molecules corresponding to natural allelic variants and homologues of an *AAP* cDNAs of the invention can be isolated based on their homology to an *AAP* of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15 using cDNA-derived probes to hybridize to homologous *AAP* sequences under stringent conditions.

"AAP variant polynucleotide" or "AAP variant nucleic acid sequence" means a nucleic acid molecule which encodes an active AAP that (1) has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native AAP, (2) a full-length native AAP lacking the signal peptide, (3) an extracellular domain of an AAP, with or without the signal peptide, or (4) any other fragment of a full-length AAP. Ordinarily, an AAP variant polynucleotide will have at least about 80% nucleic acid sequence identity, more preferably at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% nucleic

acid sequence identity and yet more preferably at least about 99% nucleic acid sequence identity with the nucleic acid sequence encoding a full-length native AAP. An AAP variant polynucleotide may encode a full-length native AAP lacking the signal peptide, an extracellular domain of an AAP, with or without the signal sequence, or any other fragment of a full-length AAP. Variants do not encompass the native nucleotide sequence.

Ordinarily, AAP variant polynucleotides are at least about 30 nucleotides in length, often at least about 60, 90, 120, 150, 180, 210, 240, 270, 300, 450, 600 nucleotides in length, more often at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to AAP-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the *AAP* sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining % nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

When nucleotide sequences are aligned, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) can be calculated as follows:

%nucleic acid sequence identity = $W/Z \cdot 100$

where

W is the number of nucleotides cored as identical matches by the sequence alignment program's or algorithm's alignment of C and D

and

Z is the total number of nucleotides in D.

When the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

2. *Stringency*

Homologs (*i.e.*, nucleic acids encoding an AAP derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

The specificity of single stranded DNA to hybridize complementary fragments is determined by the "stringency" of the reaction conditions. Hybridization stringency increases as the propensity to form DNA duplexes decreases. In nucleic acid hybridization reactions, the stringency can be chosen to either favor specific hybridizations (high stringency), which can be used to identify, for example, full-length clones from a library. Less-specific hybridizations (low stringency) can be used to identify related, but not exact, DNA molecules (homologous, but not identical) or segments.

DNA duplexes are stabilized by: (1) the number of complementary base pairs, (2) the type of base pairs, (3) salt concentration (ionic strength) of the reaction mixture, (4) the temperature of the reaction, and (5) the presence of certain organic solvents, such as formamide which decreases DNA duplex stability. In general, the longer the probe, the higher the temperature required for proper annealing. A common approach is to vary the temperature: higher relative temperatures result in more stringent reaction conditions. (Ausubel *et al.*, 1987) provide an excellent explanation of stringency of hybridization reactions.

To hybridize under "stringent conditions" describes hybridization protocols in which nucleotide sequences at least 60% homologous to each other remain hybridized. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and *p*H. The Tm is the temperature (under defined ionic strength, *p*H and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at Tm, 50% of the probes are occupied at equilibrium.

(a) *high stringency*

"Stringent hybridization conditions" conditions enable a probe, primer or oligonucleotide to hybridize only to its target sequence. Stringent conditions are sequence-dependent and will differ. Stringent conditions comprise: (1) low ionic strength and high temperature washes (*e.g.* 15 mM sodium chloride, 1.5 mM sodium citrate, 0.1 % sodium dodecyl sulfate at 50°C); (2) a denaturing agent during hybridization (*e.g.* 50% (v/v) formamide, 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50mM sodium phosphate buffer (pH 6.5; 750 mM sodium chloride, 75 mM sodium citrate at 42°C); or (3) 50% formamide. Washes typically also comprise 5X SSC (0.75 M NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. These conditions are presented as examples and are not meant to be limiting.

(b) *moderate stringency*

"Moderately stringent conditions" use washing solutions and hybridization conditions that are less stringent (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15. One example comprises hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. The temperature, ionic strength, *etc.*, can be adjusted to accommodate experimental factors such as probe length. Other moderate stringency conditions are described in (Ausubel *et al.*, 1987; Kriegler, 1990).

(c) *low stringency*

"Low stringent conditions" use washing solutions and hybridization conditions that are less stringent than those for moderate stringency (Sambrook, 1989), such that a polynucleotide will hybridize to the entire, fragments, derivatives or analogs of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5

mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency, such as those for cross-species hybridizations are described in (Ausubel *et al.*, 1987; Kriegler, 1990; Shilo and Weinberg, 1981).

3. *Conservative mutations*

In addition to naturally-occurring allelic variants of *AAP*, changes can be introduced by mutation into SEQ ID NO NOS:1, 3, 5, 7, 9, 11, 13 or 15 sequences that incur alterations in the amino acid sequences of the encoded AAP that do not alter the AAP function. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequences of the AAP without altering their biological activity, whereas an "essential" amino acid residue is required for such biological activity. For example, amino acid residues that are conserved among the AAP of the invention are predicted to be particularly non-amenable to alteration. Amino acids for which conservative substitutions can be made are well-known in the art.

Useful conservative substitutions are shown in Table A, "Preferred substitutions." Conservative substitutions whereby an amino acid of one class is replaced with another amino acid of the same type fall within the scope of the subject invention so long as the substitution does not materially alter the biological activity of the compound. If such substitutions result in a change in biological activity, then more substantial changes, indicated in Table B as exemplary are introduced and the products screened for an AAP polypeptide's biological activity.

Table A Preferred substitutions

Original residue	Exemplary substitutions	Preferred substitutions
Ala (A)	Val, Leu, Ile	Val
Arg (R)	Lys, Gln, Asn	Lys
Asn (N)	Gln, His, Lys, Arg	Gln
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp

Gly (G)	Pro, Ala	Ala
His (H)	Asn, Gln, Lys, Arg	Arg
Ile (I)	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu (L)	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys (K)	Arg, Gln, Asn	Arg
Met (M)	Leu, Phe, Ile	Leu
Phe (F)	Leu, Val, Ile, Ala, Tyr	Leu
Pro (P)	Ala	Ala
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr, Phe	Tyr
Tyr (Y)	Trp, Phe, Thr, Ser	Phe
Val (V)	Ile, Leu, Met, Phe, Ala, Norleucine	Leu

Non-conservative substitutions that effect (1) the structure of the polypeptide backbone, such as a β-sheet or α-helical conformation, (2) the charge or (3) hydrophobicity, or (4) the bulk of the side chain of the target site can modify an AAP polypeptide's function or immunological identity. Residues are divided into groups based on common side-chain properties as denoted in Table B. Non-conservative substitutions entail exchanging a member of one of these classes for another class. Substitutions may be introduced into conservative substitution sites or more preferably into non-conserved sites.

Table B Amino acid classes

Class	Amino acids
hydrophobic	Norleucine, Met, Ala, Val, Leu, Ile
neutral hydrophilic	Cys, Ser, Thr
acidic	Asp, Glu
basic	Asn, Gln, His, Lys, Arg
disrupt chain conformation	Gly, Pro
aromatic	Trp, Tyr, Phe

The variant polypeptides can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter, 1986; Zoller and Smith, 1987), cassette mutagenesis, restriction selection mutagenesis (Wells *et al.*, 1985) or other known

techniques can be performed on the cloned DNA to produce the AAP variant DNA (Ausubel *et al.*, 1987; Sambrook, 1989).

In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 45%, preferably 60%, more preferably 70%, 80%, 90%, and most preferably about 95% homologous to SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, or 15.

A mutant AAP can be assayed for blocking angiogenesis *in vitro*.

4. *Anti-sense nucleic acids*

Using antisense and sense AAP oligonucleotides can prevent AAP polypeptide expression. These oligonucleotides bind to target nucleic acid sequences, forming duplexes that block transcription or translation of the target sequence by enhancing degradation of the duplexes, terminating prematurely transcription or translation, or by other means.

Antisense or sense oligonucleotides are singe-stranded nucleic acids, either RNA or DNA, which can bind a target *AAP* mRNA (sense) or an *AAP* DNA (antisense) sequences. Anti-sense nucleic acids can be designed according to Watson and Crick or Hoogsteen base pairing rules. The anti-sense nucleic acid molecule can be complementary to the entire coding region of an *AAP* mRNA, but more preferably, to only a portion of the coding or noncoding region of an *AAP* mRNA. For example, the anti-sense oligonucleotide can be complementary to the region surrounding the translation start site of an *AAP* mRNA. Antisense or sense oligonucleotides may comprise a fragment of the AAP DNA coding region of at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. In general, antisense RNA or DNA molecules can comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 bases in length or more. Among others, (Stein and Cohen, 1988; van der Krol *et al.*, 1988a) describe methods to derive antisense or a sense oligonucleotides from a given cDNA sequence.

Examples of modified nucleotides that can be used to generate the anti-sense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-

methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the anti-sense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an anti-sense orientation such that the transcribed RNA will be complementary to a target nucleic acid of interest.

To introduce antisense or sense oligonucleotides into target cells (cells containing the target nucleic acid sequence), any gene transfer method may be used. Examples of gene transfer methods include (1) biological, such as gene transfer vectors like Epstein-Barr virus or conjugating the exogenous DNA to a ligand-binding molecule, (2) physical, such as electroporation and injection, and (3) chemical, such as $CaPO_4$ precipitation and oligonucleotide-lipid complexes.

An antisense or sense oligonucleotide is inserted into a suitable gene transfer retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Examples of suitable retroviral vectors include those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (WO 90/13641, 1990). To achieve sufficient nucleic acid molecule transcription, vector constructs in which the transcription of the anti-sense nucleic acid molecule is controlled by a strong pol II or pol III promoter are preferred.

To specify target cells in a mixed population of cells cell surface receptors that are specific to the target cells can be exploited. Antisense and sense oligonucleotides are conjugated to a ligand-binding molecule, as described in (WO 91/04753, 1991). Ligands are chosen for receptors that are specific to the target cells. Examples of suitable ligand-binding molecules include cell surface receptors, growth factors, cytokines, or other ligands that bind to cell surface receptors or molecules. Preferably, conjugation of the ligand-binding molecule does not substantially interfere with the ability of the receptors

or molecule to bind the ligand-binding molecule conjugate, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Liposomes efficiently transfer sense or an antisense oligonucleotide to cells (WO 90/10448, 1990). The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

The anti-sense nucleic acid molecule of the invention may be an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual α-units, the strands run parallel to each other (Gautier *et al.*, 1987). The anti-sense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.*, 1987a) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987b).

In one embodiment, an anti-sense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes, such as hammerhead ribozymes (Haseloff and Gerlach, 1988) can be used to catalytically cleave *AAP* mRNA transcripts and thus inhibit translation. A ribozyme specific for an AAP-encoding nucleic acid can be designed based on the nucleotide sequence of an *AAP* cDNA (*i.e.*, SEQ ID NOS:1, 3, 5, 7, 9, 11, 13 or 15). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an AAP-encoding mRNA (Cech *et al.*, U.S. Patent No. 5,116,742, 1992; Cech *et al.*, U.S. Patent No. 4,987,071, 1991). An *AAP* mRNA can also be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (Bartel and Szostak, 1993).

Alternatively, *AAP* expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an *AAP* (*e.g.*, an *AAP* promoter and/or enhancers) to form triple helical structures that prevent transcription of an *AAP* in target cells (Helene, 1991; Helene *et al.*, 1992; Maher, 1992).

Modifications of antisense and sense oligonucleotides can augment their effectiveness. Modified sugar-phosphodiester bonds or other sugar linkages (WO 91/06629, 1991), increase *in vivo* stability by conferring resistance to endogenous nucleases without disrupting binding specificity to target sequences. Other modifications

can increase the affinities of the oligonucleotides for their targets, such as covalently linked organic moieties (WO 90/10448, 1990) or poly-(L)-lysine. Other attachments modify binding specificities of the oligonucleotides for their targets, including metal complexes or intercalating (*e.g.* ellipticine) and alkylating agents.

For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (Hyrup and Nielsen, 1996). "Peptide nucleic acids" or "PNAs" refer to nucleic acid mimics (*e.g.*, DNA mimics) in that the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs allows for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols (Hyrup and Nielsen, 1996; Perry-O'Keefe *et al.*, 1996).

PNAs of an AAP can be used in therapeutic and diagnostic applications. For example, PNAs can be used as anti-sense or antigene agents for sequence-specific modulation of gene expression by inducing transcription or translation arrest or inhibiting replication. AAP PNAs may also be used in the analysis of single base pair mutations (*e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S_1 nucleases (Hyrup and Nielsen, 1996); or as probes or primers for DNA sequence and hybridization (Hyrup and Nielsen, 1996; Perry-O'Keefe *et al.*, 1996).

PNAs of an AAP can be modified to enhance their stability or cellular uptake. Lipophilic or other helper groups may be attached to PNAs, PNA-DNA dimmers formed, or the use of liposomes or other drug delivery techniques. For example, PNA-DNA chimeras can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes (*e.g.*, RNase H and DNA polymerases) to interact with the DNA portion while the PNA portion provides high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup and Nielsen, 1996). The synthesis of PNA-DNA chimeras can be performed (Finn *et al.*, 1996; Hyrup and Nielsen, 1996). For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-

deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Finn *et al.*, 1996; Hyrup and Nielsen, 1996). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Petersen *et al.*, 1976).

The oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (Lemaitre *et al.*, 1987; Letsinger *et al.*, 1989) or PCT Publication No. WO88/09810) or the blood-brain barrier (*e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (van der Krol *et al.*, 1988b) or intercalating agents (Zon, 1988). The oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, and the like.

AAP polypeptides

One aspect of the invention pertains to isolated AAP, and biologically-active portions derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-AAP Abs. In one embodiment, a native AAP can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, AAP are produced by recombinant DNA techniques. Alternative to recombinant expression, an AAP can be synthesized chemically using standard peptide synthesis techniques.

1. *Polypeptides*

An AAP polypeptide includes the amino acid sequence of an AAP whose sequences are provided in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16. The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residues shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, while still encoding a protein that maintains its AAP activities and physiological functions, or a functional fragment thereof.

2. *Variant AAP polypeptides*

In general, an AAP variant that preserves an AAP-like function and includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further includes the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above.

"AAP polypeptide variant" means an active AAP polypeptide having at least: (1) about 80% amino acid sequence identity with a full-length native sequence AAP polypeptide sequence, (2) an AAP polypeptide sequence lacking the signal peptide, (3) an extracellular domain of an AAP polypeptide, with or without the signal peptide, or (4) any other fragment of a full-length AAP polypeptide sequence. For example, AAP polypeptide variants include AAP polypeptides wherein one or more amino acid residues are added or deleted at the N- or C- terminus of the full-length native amino acid sequence. An AAP polypeptide variant will have at least about 80% amino acid sequence identity, preferably at least about 81% amino acid sequence identity, more preferably at least about 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with a full-length native sequence AAP polypeptide sequence. An AAP polypeptide variant may have a sequence lacking the signal peptide, an extracellular domain of an AAP polypeptide, with or without the signal peptide, or any other fragment of a full-length AAP polypeptide sequence. Ordinarily, AAP variant polypeptides are at least about 10 amino acids in length, often at least about 20 amino acids in length, more often at least about 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" is defined as the percentage of amino acid residues that are identical with amino acid residues in a disclosed AAP polypeptide sequence in a candidate sequence when the two sequences are aligned. To determine % amino acid identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum % sequence identity; conservative substitutions are not considered as part of the sequence identity. Amino acid sequence alignment procedures to determine percent identity are well known to those of skill in the art. Often publicly available

computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align peptide sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

When amino acid sequences are aligned, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) can be calculated as:

$$\%\text{amino acid sequence identity} = X/Y \cdot 100$$

where

X is the number of amino acid residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B

and

Y is the total number of amino acid residues in B.

If the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

3. *Isolated/purified polypeptides*

An "isolated" or "purified" polypeptide, protein or biologically active fragment is separated and/or recovered from a component of its natural environment. Contaminant components include materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous materials. Preferably, the polypeptide is purified to a sufficient degree to obtain at least 15 residues of N-terminal or internal amino acid sequence. To be substantially isolated, preparations having less than 30% by dry weight of non-AAP contaminating material (contaminants), more preferably less than 20%, 10% and most preferably less than 5% contaminants. An isolated, recombinantly-produced AAP or biologically active portion is preferably substantially free of culture medium, *i.e.*, culture medium represents less than 20%, more preferably less than about 10%, and most

preferably less than about 5% of the volume of the AAP preparation. Examples of contaminants include cell debris, culture media, and substances used and produced during *in vitro* synthesis of an AAP.

4. *Biologically active*

Biologically active portions of an AAP include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequences of an AAP (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16) that include fewer amino acids than a full-length AAP, and exhibit at least one activity of an AAP. Biologically active portions comprise a domain or motif with at least one activity of a native AAP. A biologically active portion of an AAP can be a polypeptide that is, for example, 10, 25, 50, 100 or more amino acid residues in length. Other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native AAP.

Biologically active portions of an AAP may have an amino acid sequence shown in SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, or substantially homologous to SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, and retains the functional activity of the protein of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, yet differs in amino acid sequence due to natural allelic variation or mutagenesis. Other biologically active AAP may comprise an amino acid sequence at least 45% homologous to the amino acid sequence of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16, and retains the functional activity of native AAP.

5. *Determining homology between two or more sequences*

"AAP variant" means an active AAP having at least: (1) about 80% amino acid sequence identity with a full-length native sequence AAP sequence, (2) an AAP sequence lacking the signal peptide, (3) an extracellular domain of an AAP, with or without the signal peptide, or (4) any other fragment of a full-length AAP sequence. For example, AAP variants include an AAP wherein one or more amino acid residues are added or deleted at the N- or C- terminus of the full-length native amino acid sequence. An AAP variant will have at least about 80% amino acid sequence identity, preferably at least about 81% amino acid sequence identity, more preferably at least about 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% amino acid sequence identity and most preferably at least about 99% amino acid sequence identity with a full-length native sequence AAP sequence. An AAP variant may have a

sequence lacking the signal peptide, an extracellular domain of an AAP, with or without the signal peptide, or any other fragment of a full-length AAP sequence. Ordinarily, AAP variant polypeptides are at least about 10 amino acids in length, often at least about 20 amino acids in length, more often at least about 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" is defined as the percentage of amino acid residues that are identical with amino acid residues in a disclosed AAP sequence in a candidate sequence when the two sequences are aligned. To determine % amino acid identity, sequences are aligned and if necessary, gaps are introduced to achieve the maximum % sequence identity; conservative substitutions are not considered as part of the sequence identity. Amino acid sequence alignment procedures to determine percent identity are well known to those of skill in the art. Often publicly available computer software such as BLAST, BLAST2, ALIGN2 or Megalign (DNASTAR) software is used to align peptide sequences. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

When amino acid sequences are aligned, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) can be calculated as:

$$\%\text{amino acid sequence identity} = X/Y \cdot 100$$

where

X is the number of amino acid residues scored as identical matches by the sequence alignment program's or algorithm's alignment of A and B

and

Y is the total number of amino acid residues in B.

If the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

6. *Chimeric and fusion proteins*

Fusion polypeptides are useful in expression studies, cell-localization, bioassays, and AAP purification. An AAP "chimeric protein" or "fusion protein" comprises an AAP fused to a non-AAP polypeptide. A non-AAP polypeptide is not substantially homologous to an AAP (SEQ ID NOS:2, 4, 6, 8, 10, 12, 14 or 16). An AAP fusion protein may include any portion to an entire AAP, including any number of the biologically active portions. An AAP may be fused to the C-terminus of the GST (glutathione S-transferase) sequences. Such fusion proteins facilitate the purification of a recombinant AAP. In certain host cells, (*e.g.* mammalian), heterologous signal sequences fusions may ameliorate AAP expression and/or secretion. Additional exemplary fusions are presented in Table C.

Other fusion partners can adapt an AAP therapeutically. Fusions with members of the immunoglobulin (Ig) protein family are useful in therapies that inhibit an AAP ligand or substrate interactions, consequently suppressing an AAP-mediated signal transduction *in vivo*. Such fusions, incorporated into pharmaceutical compositions, may be used to treat proliferative and differentiation disorders, as well as modulating cell survival. An AAP-Ig fusion polypeptides can also be used as immunogens to produce an anti-AAP Abs in a subject, to purify AAP ligands, and to screen for molecules that inhibit interactions of an AAP with other molecules.

Fusion proteins can be easily created using recombinant methods. A nucleic acid encoding an AAP can be fused in-frame with a non-AAP encoding nucleic acid, to an AAP NH_2- or COO- -terminus, or internally. Fusion genes may also be synthesized by conventional techniques, including automated DNA synthesizers. PCR amplification using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (Ausubel *et al.*, 1987) is also useful. Many vectors are commercially available that facilitate sub-cloning an *AAP* in-frame to a fusion moiety.

Table C Useful non-AAP fusion polypeptides

Reporter	*in vitro*	*in vivo*	Notes	Reference

Human growth hormone (hGH)	Radioimmuno-assay	none	Expensive, insensitive, narrow linear range.	(Selden *et al.*, 1986)
β-glucu-ronidase (GUS)	Colorimetric, fluorescent, or chemi-luminescent	colorimetric (histo-chemical staining with X-gluc)	sensitive, broad linear range, non-iostopic.	(Gallagher, 1992)
Green fluorescent protein (GFP) and related molecules (RFP, BFP, AAP, *etc.*)	Fluorescent	fluorescent	can be used in live cells; resists photo-bleaching	(Chalfie *et al.*, 1994)
Luciferase (firefly)	bioluminsecent	Bio-luminescent	protein is unstable, difficult to reproduce, signal is brief	(de Wet *et al.*, 1987)
Chloramphenicol acetyltransferase (CAT)	Chromato-graphy, differential extraction, fluorescent, or immunoassay	none	Expensive radioactive substrates, time-consuming, insensitive, narrow linear range	(Gorman *et al.*, 1982)
β-galacto-sidase	colorimetric, fluorescence, chemi-luminscence	colorimetric (histochemical staining with X-gal), bio-luminescent in live cells	sensitive, broad linear range; some cells have high endogenous activity	(Alam and Cook, 1990)
Secrete alkaline phosphatase (SEAP)	colorimetric, bioluminescent, chemi-luminescent	none	Chem-iluminscence assay is sensitive and broad linear range; some cells have endogenouse alkaline phosphatase activity	(Berger *et al.*, 1988)

Therapeutic applications of AAP

1. *Agonists and antagonists*

"Antagonist" includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of an endogenous AAP. Similarly, "agonist" includes any molecule that mimics a biological activity of an endogenous AAP. Molecules that can act as agonists or antagonists include Abs or antibody fragments, fragments or variants of an endogenous AAP, peptides, antisense oligonucleotides, small organic molecules, *etc.*

2. *Identifying antagonists and agonists*

To assay for antagonists, an AAP is added to, or expressed in, a cell along with the compound to be screened for a particular activity. If the compound inhibits the activity of interest in the presence of an AAP, that compound is an antagonist to the AAP; if an AAP activity is enhanced, the compound is an agonist.

(a) *Specific examples of potential antagonists and agonist*

Any molecule that alters AAP cellular effects is a candidate antagonist or agonist. Screening techniques well known to those skilled in the art can identify these molecules. Examples of antagonists and agonists include: (1) small organic and inorganic compounds, (2) small peptides, (3) Abs and derivatives, (4) polypeptides closely related to an AAP, (5) antisense DNA and RNA, (6) ribozymes, (7) triple DNA helices and (8) nucleic acid aptamers.

Small molecules that bind to an AAP active site or other relevant part of the polypeptide and inhibit the biological activity of the AAP are antagonists. Examples of small molecule antagonists include small peptides, peptide-like molecules, preferably soluble, and synthetic non-peptidyl organic or inorganic compounds. These same molecules, if they enhance an AAP activity, are examples of agonists.

Almost any antibody that affects an AAP's function is a candidate antagonist, and occasionally, agonist. Examples of antibody antagonists include polyclonal, monoclonal, single-chain, anti-idiotypic, chimeric Abs, or humanized versions of such Abs or fragments. Abs may be from any species in which an immune response can be raised. Humanized Abs are also contemplated.

Alternatively, a potential antagonist or agonist may be a closely related protein, for example, a mutated form of an AAP that recognizes an AAP-interacting protein but imparts no effect, thereby competitively inhibiting AAP action. Alternatively, a mutated AAP may be constitutively activated and may act as an agonist.

Antisense RNA or DNA constructs can be effective antagonists. Antisense RNA or DNA molecules block function by inhibiting translation by hybridizing to targeted mRNA. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which depend on polynucleotide binding to DNA or RNA. For example, the 5' coding portion of an *AAP* sequence is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix) (Beal and Dervan, 1991; Cooney *et al.*, 1988; Lee *et al.*, 1979), thereby preventing transcription and the production of the AAP. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the AAP (antisense) (Cohen, 1989; Okano *et al.*, 1991). These oligonucleotides can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the AAP. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, *e.g.*, between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques (WO 97/33551, 1997; Rossi, 1994).

To inhibit transcription, triple-helix nucleic acids that are single-stranded and comprise deoxynucleotides are useful antagonists. These oligonucleotides are designed such that triple-helix formation via Hoogsteen base-pairing rules is promoted, generally requiring stretches of purines or pyrimidines (WO 97/33551, 1997).

Aptamers are short oligonucleotide sequences that can be used to recognize and specifically bind almost any molecule. The systematic evolution of ligands by exponential enrichment (SELEX) process (Ausubel *et al.*, 1987; Ellington and Szostak, 1990; Tuerk and Gold, 1990) is powerful and can be used to find such aptamers. Aptamers have many diagnostic and clinical uses; almost any use in which an antibody has been used clinically or diagnostically, aptamers too may be used. In addition, they are cheaper to make once they have been identified, and can be easily applied in a variety

of formats, including administration in pharmaceutical compositions, in bioassays, and diagnostic tests (Jayasena, 1999).

Anti-AAP Abs

The invention encompasses Abs and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any AAP epitopes.

"Antibody" (Ab) comprises single Abs directed against an AAP (anti-AAP Ab; including agonist, antagonist, and neutralizing Abs), anti-AAP Ab compositions with poly-epitope specificity, single chain anti-AAP Abs, and fragments of anti-AAP Abs. A "monoclonal antibody" is obtained from a population of substantially homogeneous Abs, *i.e.*, the individual Abs comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts. Exemplary Abs include polyclonal (pAb), monoclonal (mAb), humanized, bi-specific (bsAb), and heteroconjugate Abs.

1. *Polyclonal Abs (pAbs)*

Polyclonal Abs can be raised in a mammalian host, for example, by one or more injections of an immunogen and, if desired, an adjuvant. Typically, the immunogen and/or adjuvant are injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunogen may include an AAP or a fusion protein. Examples of adjuvants include Freund's complete and monophosphoryl Lipid A synthetic-trehalose dicorynomycolate (MPL-TDM). To improve the immune response, an immunogen may be conjugated to a protein that is immunogenic in the host, such as keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Protocols for antibody production are described by (Ausubel *et al.*, 1987; Harlow and Lane, 1988). Alternatively, pAbs may be made in chickens, producing IgY molecules (Schade *et al.*, 1996).

2. *Monoclonal Abs (mAbs)*

Anti-AAP mAbs may be prepared using hybridoma methods (Milstein and Cuello, 1983). Hybridoma methods comprise at least four steps: (1) immunizing a host, or lymphocytes from a host; (2) harvesting the mAb secreting (or potentially secreting) lymphocytes, (3) fusing the lymphocytes to immortalized cells, and (4) selecting those cells that secrete the desired (anti-AAP) mAb.

A mouse, rat, guinea pig, hamster, or other appropriate host is immunized to elicit lymphocytes that produce or are capable of producing Abs that will specifically bind to the immunogen. Alternatively, the lymphocytes may be immunized *in vitro*. If human cells are desired, peripheral blood lymphocytes (PBLs) are generally used; however, spleen cells or lymphocytes from other mammalian sources are preferred. The immunogen typically includes an AAP or a fusion protein.

The lymphocytes are then fused with an immortalized cell line to form hybridoma cells, facilitated by a fusing agent such as polyethylene glycol (Goding, 1996). Rodent, bovine, or human myeloma cells immortalized by transformation may be used, or rat or mouse myeloma cell lines. Because pure populations of hybridoma cells and not unfused immortalized cells are preferred, the cells after fusion are grown in a suitable medium that contains one or more substances that inhibit the growth or survival of unfused, immortalized cells. A common technique uses parental cells that lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT). In this case, hypoxanthine, aminopterin and thymidine are added to the medium (HAT medium) to prevent the growth of HGPRT-deficient cells while permitting hybridomas to grow.

Preferred immortalized cells fuse efficiently, can be isolated from mixed populations by selecting in a medium such as HAT, and support stable and high-level expression of antibody after fusion. Preferred immortalized cell lines are murine myeloma lines, available from the American Type Culture Collection (Manassas, VA). Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human mAbs (Kozbor *et al.*, 1984; Schook, 1987).

Because hybridoma cells secrete antibody extracellularly, the culture media can be assayed for the presence of mAbs directed against an AAP (anti-AAP mAbs). Immunoprecipitation or *in vitro* binding assays, such as radio immunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA), measure the binding specificity of mAbs (Harlow and Lane, 1988; Harlow and Lane, 1999), including Scatchard analysis (Munson and Rodbard, 1980).

Anti-AAP mAb secreting hybridoma cells may be isolated as single clones by limiting dilution procedures and sub-cultured (Goding, 1996). Suitable culture media include Dulbecco's Modified Eagle's Medium, RPMI-1640, or if desired, a protein-free

or -reduced or serum-free medium (*e.g.*, Ultra DOMA PF or HL-1; Biowhittaker; Walkersville, MD). The hybridoma cells may also be grown *in vivo* as ascites.

The mAbs may be isolated or purified from the culture medium or ascites fluid by conventional Ig purification procedures such as protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, ammonium sulfate precipitation or affinity chromatography (Harlow and Lane, 1988; Harlow and Lane, 1999).

The mAbs may also be made by recombinant methods (U.S. Patent No. 4166452, 1979). DNA encoding anti-AAP mAbs can be readily isolated and sequenced using conventional procedures, *e.g.*, using oligonucleotide probes that specifically bind to murine heavy and light antibody chain genes, to probe preferably DNA isolated from anti-AAP-secreting mAb hybridoma cell lines. Once isolated, the isolated DNA fragments are sub-cloned into expression vectors that are then transfected into host cells such as simian COS-7 cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce Ig protein, to express mAbs. The isolated DNA fragments can be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homológous murine sequences (U.S. Patent No. 4816567, 1989; Morrison *et al.*, 1987), or by fusing the Ig coding sequence to all or part of the coding sequence for a non-Ig polypeptide. Such a non-Ig polypeptide can be substituted for the constant domains of an antibody, or can be substituted for the variable domains of one antigen-combining site to create a chimeric bivalent antibody.

3. *Monovalent Abs*

The Abs may be monovalent Abs that consequently do not cross-link with each other. For example, one method involves recombinant expression of Ig light chain and modified heavy chain. Heavy chain truncations generally at any point in the F_c region will prevent heavy chain cross-linking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted, preventing crosslinking. *In vitro* methods are also suitable for preparing monovalent Abs. Abs can be digested to produce fragments, such as F_{ab} fragments (Harlow and Lane, 1988; Harlow and Lane, 1999).

4. *Humanized and human Abs*

Anti-AAP Abs may further comprise humanized or human Abs. Humanized forms of non-human Abs are chimeric Igs, Ig chains or fragments (such as F_v, F_{ab}, $F_{ab'}$,

$F_{(ab')2}$ or other antigen-binding subsequences of Abs) that contain minimal sequence derived from non-human Ig.

Generally, a humanized antibody has one or more amino acid residues introduced from a non-human source. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization is accomplished by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody (Jones *et al.*, 1986; Riechmann *et al.*, 1988; Verhoeyen *et al.*, 1988). Such "humanized" Abs are chimeric Abs (U.S. Patent No. 4816567, 1989), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized Abs are typically human Abs in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent Abs. Humanized Abs include human Igs (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit, having the desired specificity, affinity and capacity. In some instances, corresponding non-human residues replace F_v framework residues of the human Ig. Humanized Abs may comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody comprises substantially all of at least one, and typically two, variable domains, in which most if not all of the CDR regions correspond to those of a non-human Ig and most if not all of the FR regions are those of a human Ig consensus sequence. The humanized antibody optimally also comprises at least a portion of an Ig constant region (F_c), typically that of a human Ig (Jones *et al.*, 1986; Presta, 1992; Riechmann *et al.*, 1988).

Human Abs can also be produced using various techniques, including phage display libraries (Hoogenboom *et al.*, 1991; Marks *et al.*, 1991) and the preparation of human mAbs (Boerner *et al.*, 1991; Reisfeld and Sell, 1985). Similarly, introducing human Ig genes into transgenic animals in which the endogenous Ig genes have been partially or completely inactivated can be exploited to synthesize human Abs. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire (U.S. Patent No. 5545807, 1996; U.S. Patent No. 5545806, 1996; U.S. Patent No.

5569825, 1996; U.S. Patent No. 5633425, 1997; U.S. Patent No. 5661016, 1997; U.S. Patent No. 5625126, 1997; Fishwild *et al.*, 1996; Lonberg and Huszar, 1995; Lonberg *et al.*, 1994; Marks *et al.*, 1992).

5. *Bi-specific mAbs*

Bi-specific Abs are monoclonal, preferably human or humanized, that have binding specificities for at least two different antigens. For example, a binding specificity is an AAP; the other is for any antigen of choice, preferably a cell-surface protein or receptor or receptor subunit.

Traditionally, the recombinant production of bi-specific Abs is based on the co-expression of two Ig heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, 1983). Because of the random assortment of Ig heavy and light chains, the resulting hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the desired bi-specific structure. The desired antibody can be purified using affinity chromatography or other techniques (WO 93/08829, 1993; Traunecker *et al.*, 1991).

To manufacture a bi-specific antibody (Suresh *et al.*, 1986), variable domains with the desired antibody-antigen combining sites are fused to Ig constant domain sequences. The fusion is preferably with an Ig heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. Preferably, the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding is in at least one of the fusions. DNAs encoding the Ig heavy-chain fusions and, if desired, the Ig light chain, are inserted into separate expression vectors and are co-transfected into a suitable host organism.

The interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers that are recovered from recombinant cell culture (WO 96/27011, 1996). The preferred interface comprises at least part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.* tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.* alanine or threonine). This

mechanism increases the yield of the heterodimer over unwanted end products such as homodimers.

Bi-specific Abs can be prepared as full length Abs or antibody fragments (*e.g.* $F_{(ab')2}$ bi-specific Abs). One technique to generate bi-specific Abs exploits chemical linkage. Intact Abs can be proteolytically cleaved to generate $F_{(ab')2}$ fragments (Brennan *et al.*, 1985). Fragments are reduced with a dithiol complexing agent, such as sodium arsenite, to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The generated $F_{ab'}$ fragments are then converted to thionitrobenzoate (TNB) derivatives. One of the $F_{ab'}$-TNB derivatives is then reconverted to the $F_{ab'}$-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other $F_{ab'}$-TNB derivative to form the bi-specific antibody. The produced bi-specific Abs can be used as agents for the selective immobilization of enzymes.

$F_{ab'}$ fragments may be directly recovered from *E. coli* and chemically coupled to form bi-specific Abs. For example, fully humanized bi-specific $F_{(ab')2}$ Abs can be produced (Shalaby *et al.*, 1992). Each $F_{ab'}$ fragment is separately secreted from *E. coli* and directly coupled chemically *in vitro*, forming the bi-specific antibody.

Various techniques for making and isolating bi-specific antibody fragments directly from recombinant cell culture have also been described. For example, leucine zipper motifs can be exploited (Kostelny *et al.*, 1992). Peptides from the *Fos* and *Jun* proteins are linked to the $F_{ab'}$ portions of two different Abs by gene fusion. The antibody homodimers are reduced at the hinge region to form monomers and then re-oxidized to form antibody heterodimers. This method can also produce antibody homodimers. The "diabody" technology (Holliger *et al.*, 1993) provides an alternative method to generate bi-specific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker that is too short to allow pairing between the two domains on the same chain. The V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, forming two antigen-binding sites. Another strategy for making bi-specific antibody fragments is the use of single-chain F_v (sF_v) dimers (Gruber *et al.*, 1994). Abs with more than two valencies are also contemplated, such as tri-specific Abs (Tutt *et al.*, 1991).

Exemplary bi-specific Abs may bind to two different epitopes on a given AAP. Alternatively, cellular defense mechanisms can be restricted to a particular cell expressing the particular AAP: an anti-AAP arm may be combined with an arm that binds to a leukocyte triggering molecule, such as a T-cell receptor molecule (*e.g.* CD2, CD3, CD28, or B7), or to F_c receptors for IgG ($F_c\gamma R$), such as $F_c\gamma RI$ (CD64), $F_c\gamma RII$ (CD32) and $F_c\gamma RIII$ (CD16). Bi-specific Abs may also be used to target cytotoxic agents to cells that express a particular AAP. These Abs possess an AAP-binding arm and an arm that binds a cytotoxic agent or a radionuclide chelator.

6. *Heteroconjugate Abs*

Heteroconjugate Abs, consisting of two covalently joined Abs, have been proposed to target immune system cells to unwanted cells (4,676,980, 1987) and for treatment of human immunodeficiency virus (HIV) infection (WO 91/00360, 1991; WO 92/20373, 1992). Abs prepared *in vitro* using synthetic protein chemistry methods, including those involving cross-linking agents, are contemplated. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents include iminothiolate and methyl-4-mercaptobutyrimidate (4,676,980, 1987).

7. *Immunoconjugates*

Immunoconjugates may comprise an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin or fragment of bacterial, fungal, plant, or animal origin), or a radioactive isotope (*i.e.*, a radioconjugate).

Useful enzymatically-active toxins and fragments include Diphtheria A chain, non-binding active fragments of Diphtheria toxin, exotoxin A chain from *Pseudomonas aeruginosa,* ricin A chain, abrin A chain, modeccin A chain, α-sarcin, *Aleurites fordii* proteins, Dianthin proteins, *Phytolaca americana* proteins, *Momordica charantia* inhibitor, curcin, crotin, *Sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated Abs, such as ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, and ^{186}Re.

Conjugates of the antibody and cytotoxic agent are made using a variety of bi-functional protein-coupling agents, such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bi-functional derivatives of imidoesters (such as

dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), *bis*-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), *bis*-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6- diisocyanate), and *bis*-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared (Vitetta *et al.*, 1987). ^{14}C-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugating radionuclide to antibody (WO 94/11026, 1994).

In another embodiment, the antibody may be conjugated to a "receptor" (such as streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a streptavidin "ligand" (*e.g.*, biotin) that is conjugated to a cytotoxic agent (*e.g.*, a radionuclide).

8. *Effector function engineering*

The antibody can be modified to enhance its effectiveness in treating a disease, such as cancer. For example, cysteine residue(s) may be introduced into the F_c region, thereby allowing interchain disulfide bond formation in this region. Such homodimeric Abs may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC) (Caron *et al.*, 1992; Shopes, 1992). Homodimeric Abs with enhanced anti-tumor activity can be prepared using hetero-bifunctional cross-linkers (Wolff *et al.*, 1993). Alternatively, an antibody engineered with dual F_c regions may have enhanced complement lysis (Stevenson *et al.*, 1989).

9. *Immunoliposomes*

Liposomes containing the antibody may also be formulated (U.S. Patent No. 4485045, 1984; U.S. Patent No. 4544545, 1985; U.S. Patent No. 5013556, 1991; Eppstein *et al.*, 1985; Hwang *et al.*, 1980). Useful liposomes can be generated by a reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG- PE). Such preparations are extruded through filters of defined pore size to yield liposomes with a desired diameter. $F_{ab'}$ fragments of the antibody can be conjugated to the liposomes (Martin and Papahadjopoulos, 1982) via a disulfide-interchange reaction. A

chemotherapeutic agent, such as Doxorubicin, may also be contained in the liposome (Gabizon *et al.*, 1989). Other useful liposomes with different compositions are contemplated.

10. *Diagnostic applications of Abs directed against an AAP*

Anti-AAP Abs can be used to localize and/or quantitate anAAP (*e.g.*, for use in measuring levels of an AAP within tissue samples or for use in diagnostic methods, *etc.*). Anti-AAP epitope Abs can be utilized as pharmacologically-active compounds.

Anti-AAP Abs can be used to isolate an AAP by standard techniques, such as immunoaffinity chromatography or immunoprecipitation. These approaches facilitate purifying an endogenous AAP antigen-containing polypeptides from cells and tissues. These approaches, as well as others, can be used to detect an AAP in a sample to evaluate the abundance and pattern of expression of the antigenic protein. Anti-AAP Abs can be used to monitor protein levels in tissues as part of a clinical testing procedure; for example, to determine the efficacy of a given treatment regimen. Coupling the antibody to a detectable substance (label) allows detection of Ab-antigen complexes. Classes of labels include fluorescent, luminescent, bioluminescent, and radioactive materials, enzymes and prosthetic groups. Useful labels include horseradish peroxidase, alkaline phosphatase, β-galactosidase, acetylcholinesterase, streptavidin/biotin, avidin/biotin, umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride, phycoerythrin, luminol, luciferase, luciferin, aequorin, and ^{125}I, ^{131}I, ^{35}S or ^{3}H.

11. *Antibody therapeutics*

Abs of the invention, including polyclonal, monoclonal, humanized and fully human Abs, can be used therapeutically. Such agents will generally be employed to treat or prevent a disease or pathology in a subject. An antibody preparation, preferably one having high antigen specificity and affinity generally mediates an effect by binding the target epitope(s). Generally, administration of such Abs may mediate one of two effects: (1) the antibody may prevent ligand binding, eliminating endogenous ligand binding and subsequent signal transduction, or (2) the antibody elicits a physiological result by binding an effector site on the target molecule, initiating signal transduction.

A therapeutically effective amount of an antibody relates generally to the amount needed to achieve a therapeutic objective, epitope binding affinity, administration rate,

and depletion rate of the antibody from a subject. Common ranges for therapeutically effective doses may be, as a nonlimiting example, from about 0.1 mg/kg body weight to about 50 mg/kg body weight. Dosing frequencies may range, for example, from twice daily to once a week.

12. *Pharmaceutical compositions of Abs*

Anti-AAP Abs, as well as other AAP interacting molecules (such as aptamers) identified in other assays, can be administered in pharmaceutical compositions to treat various disorders. Principles and considerations involved in preparing such compositions, as well as guidance in the choice of components can be found in (de Boer, 1994; Gennaro, 2000; Lee, 1990).

Since some AAP are intracellular, Abs that are internalized are preferred used when whole Abs are used as inhibitors. Liposomes may also be used as a delivery vehicle for intracellular introduction. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the epitope is preferred. For example, peptide molecules can be designed that bind a preferred epitope based on the variable-region sequences of a useful antibody. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology (Marasco *et al.*, 1993). Formulations may also contain more than one active compound for a particular treatment, preferably those with activities that do not adversely affect each other. The composition may comprise an agent that enhances function, such as a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent.

The active ingredients can also be entrapped in microcapsules prepared by coacervation techniques or by interfacial polymerization; for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions.

The formulations to be used for *in vivo* administration are highly preferred to be sterile. This is readily accomplished by filtration through sterile filtration membranes or any of a number of techniques.

Sustained-release preparations may also be prepared, such as semi-permeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in

the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (Boswell and Scribner, U.S. Patent No. 3,773,919, 1973), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as injectable microspheres composed of lactic acid-glycolic acid copolymer, and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods and may be preferred.

AAP recombinant expression vectors and host cells

Vectors are tools used to shuttle DNA between host cells or as a means to express a nucleotide sequence. Some vectors function only in prokaryotes, while others function in both prokaryotes and eukaryotes, enabling large-scale DNA preparation from prokaryotes for expression in eukaryotes. Inserting the DNA of interest, such as an AAP nucleotide sequence or a fragment, is accomplished by ligation techniques and/or mating protocols well-known to the skilled artisan. Such DNA is inserted such that its integration does not disrupt any necessary components of the vector. In the case of vectors that are used to express the inserted DNA protein, the introduced DNA is operably-linked to the vector elements that govern its transcription and translation.

Vectors can be divided into two general classes: Cloning vectors are replicating plasmid or phage with regions that are non-essential for propagation in an appropriate host cell, and into which foreign DNA can be inserted; the foreign DNA is replicated and propagated as if it were a component of the vector. An expression vector (such as a plasmid, yeast, or animal virus genome) is used to introduce foreign genetic material into a host cell or tissue in order to transcribe and translate the foreign DNA. In expression vectors, the introduced DNA is operably-linked to elements, such as promoters, that signal to the host cell to transcribe the inserted DNA. Some promoters are exceptionally useful, such as inducible promoters that control gene transcription in response to specific factors. Operably-linking an *AAP* or anti-sense construct to an inducible promoter can control the expression of an *AAP* or fragments, or anti-sense constructs. Examples of classic inducible promoters include those that are responsive to α-interferon, heat-shock,

heavy metal ions, and steroids such as glucocorticoids (Kaufman, 1990) and tetracycline. Other desirable inducible promoters include those that are not endogenous to the cells in which the construct is being introduced, but, however, is responsive in those cells when the induction agent is exogenously supplied.

Vectors have many difference manifestations. A "plasmid" is a circular double stranded DNA molecule into which additional DNA segments can be introduced. Viral vectors can accept additional DNA segments into the viral genome. Certain vectors are capable of autonomous replication in a host cell (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. In general, useful expression vectors are often plasmids. However, other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) are contemplated.

Recombinant expression vectors that comprise an *AAP* (or fragments) regulate an *AAP* transcription by exploiting one or more host cell-responsive (or that can be manipulated *in vitro*) regulatory sequences that is operably-linked to an *AAP*. "Operably-linked" indicates that a nucleotide sequence of interest is linked to regulatory sequences such that expression of the nucleotide sequence is achieved.

Vectors can be introduced in a variety of organisms and/or cells (Table D). Alternatively, the vectors can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Table D Examples of hosts for cloning or expression

Organisms	Examples	Sources and References*
Prokaryotes		
Enterobacteriaceae	*E. coli*	
	K 12 strain MM294	ATCC 31,446
	X1776	ATCC 31,537
	W3110	ATCC 27,325
	K5 772	ATCC 53,635
	Enterobacter	
	Erwinia	
	Klebsiella	
	Proteus	

Table D Examples of hosts for cloning or expression

Organisms	Examples	Sources and References*
	Salmonella (*S. tyhpimurium*)	
	Serratia (*S. marcescans*)	
	Shigella	
	Bacilli (B. *subtilis* and *B. licheniformis*)	
	Pseudomonas (P. *aeruginosa*)	
	Streptomyces	
Eukaryotes		
Yeasts	*Saccharomyces cerevisiae*	
	Schizosaccharomyces pombe	
	Kluyveromyces *K. lactis* MW98-8C, CBS683, CBS4574 *K. fragilis* *K. bulgaricus* *K. wickeramii* *K. waltii* *K. drosophilarum* *K. thermotolerans* *K. marxianus; yarrowia*	(Fleer *et al.*, 1991) (de Louvencourt *et al.*, 1983) ATCC 12,424 ATCC 16,045 ATCC 24,178 ATCC 56,500 ATCC 36,906 (EPO 402226, 1990)
	Pichia pastoris	(Sreekrishna *et al.*, 1988)
	Candida	
	Trichoderma reesia	
	Neurospora crassa	(Case *et al.*, 1979)
	Torulopsis	
	Rhodotorula	
	Schwanniomyces (*S. occidentalis*)	
Filamentous Fungi	*Neurospora*	
	Penicillium	
	Tolypocladium	(WO 91/00357, 1991)
	Aspergillus (*A. nidulans* and *A. niger*)	(Kelly and Hynes, 1985; Tilburn *et al.*, 1983; Yelton *et al.*, 1984)
Invertebrate cells	*Drosophila* S2	
	Spodoptera Sf9	
Vertebrate cells	Chinese Hamster Ovary (CHO)	
	simian COS COS-7	ATCC CRL 1651
	HEK 293	

*Unreferenced cells are generally available from American Type Culture Collection (Manassas, VA).

Vector choice is dictated by the organism or cells being used and the desired fate of the vector. Vectors may replicate once in the target cells, or may be "suicide" vectors. In general, vectors comprise signal sequences, origins of replication, marker genes, enhancer elements, promoters, and transcription termination sequences. The choice of these elements depends on the organisms in which the vector will be used and are easily determined. Some of these elements may be conditional, such as an inducible or conditional promoter that is turned "on" when conditions are appropriate. Examples of inducible promoters include those that are tissue-specific, which relegate expression to certain cell types, steroid-responsive, or heat-shock reactive. Some bacterial repression systems, such as the *lac* operon, have been exploited in mammalian cells and transgenic animals (Fieck *et al.*, 1992; Wyborski *et al.*, 1996; Wyborski and Short, 1991). Vectors often use a selectable marker to facilitate identifying those cells that have incorporated the vector. Many selectable markers are well known in the art for the use with prokaryotes, usually antibiotic-resistance genes or the use of autotrophy and auxotrophy mutants.

Using antisense and sense AAP oligonucleotides can prevent an AAP polypeptide expression. These oligonucleotides bind to target nucleic acid sequences, forming duplexes that block transcription or translation of the target sequence by enhancing degradation of the duplexes, terminating prematurely transcription or translation, or by other means.

Antisense or sense oligonucleotides are singe-stranded nucleic acids, either RNA or DNA, which can bind a target AAP mRNA (sense) or an AAP DNA (antisense) sequences. According to the present invention, antisense or sense oligonucleotides comprise a fragment of an AAP DNA coding region of at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. In general, antisense RNA or DNA molecules can comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 bases in length or more. Among others, (Stein and Cohen, 1988; van der Krol *et al.*, 1988a) describe methods to derive antisense or a sense oligonucleotides from a given cDNA sequence.

Modifications of antisense and sense oligonucleotides can augment their effectiveness. Modified sugar-phosphodiester bonds or other sugar linkages (WO

91/06629, 1991), increase *in vivo* stability by conferring resistance to endogenous nucleases without disrupting binding specificity to target sequences. Other modifications can increase the affinities of the oligonucleotides for their targets, such as covalently linked organic moieties (WO 90/10448, 1990) or poly-(L)-lysine. Other attachments modify binding specificities of the oligonucleotides for their targets, including metal complexes or intercalating (*e.g.* ellipticine) and alkylating agents.

To introduce antisense or sense oligonucleotides into target cells (cells containing the target nucleic acid sequence), any gene transfer method may be used and are well known to those of skill in the art. Examples of gene transfer methods include 1) biological, such as gene transfer vectors like Epstein-Barr virus or conjugating the exogenous DNA to a ligand-binding molecule (WO 91/04753, 1991), 2) physical, such as electroporation, and 3) chemical, such as $CaPO_4$ precipitation and oligonucleotide-lipid complexes (WO 90/10448, 1990).

The terms "host cell" and "recombinant host cell" are used interchangeably. Such terms refer not only to a particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are well known in the art. The choice of host cell will dictate the preferred technique for introducing the nucleic acid of interest. Table E, which is not meant to be limiting, summarizes many of the known techniques in the art. Introduction of nucleic acids into an organism may also be done with *ex vivo* techniques that use an *in vitro* method of transfection, as well as established genetic techniques, if any, for that particular organism.

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
Prokaryotes (bacteria)	Calcium chloride	(Cohen *et al.*, 1972; Hanahan, 1983; Mandel and Higa, 1970)	
	Electroporation	(Shigekawa and Dower, 1988)	
Eukaryotes			

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
Mammalian cells	Calcium phosphate transfection	*N*-(2-Hydroxyethyl)piperazine-*N*'-(2-ethanesulfonic acid (HEPES) buffered saline solution (Chen and Okayama, 1988; Graham and van der Eb, 1973; Wigler *et al.*, 1978) BES (*N,N*-bis(2-hydroxyethyl)-2-aminoethanesulfonic acid) buffered solution (Ishiura *et al.*, 1982)	Cells may be "shocked" with glycerol or dimethylsulfoxide (DMSO) to increase transfection efficiency (Ausubel *et al.*, 1987).
	Diethylaminoethyl (DEAE)-Dextran transfection	(Fujita *et al.*, 1986; Lopata *et al.*, 1984; Selden *et al.*, 1986)	Most useful for transient, but not stable, transfections. Chloroquine can be used to increase efficiency.
	Electroporation	(Neumann *et al.*, 1982; Potter, 1988; Potter *et al.*, 1984; Wong and Neumann, 1982)	Especially useful for hard-to-transfect lymphocytes.
	Cationic lipid reagent transfection	(Elroy-Stein and Moss, 1990; Felgner *et al.*, 1987; Rose *et al.*, 1991; Whitt *et al.*, 1990)	Applicable to both *in vivo* and *in vitro* transfection.
	Retroviral	Production exemplified by (Cepko *et al.*, 1984; Miller and Buttimore, 1986; Pear *et al.*, 1993) Infection *in vitro* and *in vivo*: (Austin and Cepko, 1990; Bodine *et al.*, 1991; Fekete and Cepko, 1993; Lemischka *et al.*, 1986; Turner *et al.*, 1990; Williams *et al.*, 1984)	Lengthy process, many packaging lines available at ATCC. Applicable to both *in vivo* and *in vitro* transfection.
	Polybrene	(Chaney *et al.*, 1986; Kawai and Nishizawa, 1984)	
	Microinjection	(Capecchi, 1980)	Can be used to establish cell lines carrying integrated copies of AAP DNA sequences.

Table E Methods to introduce nucleic acid into cells

Cells	Methods	References	Notes
	Protoplast fusion	(Rassoulzadegan *et al.*, 1982; Sandri-Goldin *et al.*, 1981; Schaffner, 1980)	
Insect cells (*in vitro*)	Baculovirus systems	(Luckow, 1991; Miller, 1988; O'Reilly *et al.*, 1992)	Useful for *in vitro* production of proteins with eukaryotic modifications.
Yeast	Electroporation	(Becker and Guarente, 1991)	
	Lithium acetate	(Gietz *et al.*, 1998; Ito *et al.*, 1983)	
	Spheroplast fusion	(Beggs, 1978; Hinnen *et al.*, 1978)	Laborious, can produce aneuploids.
Plant cells (general reference: (Hansen and Wright, 1999))	Agrobacterium transformation	(Bechtold and Pelletier, 1998; Escudero and Hohn, 1997; Hansen and Chilton, 1999; Touraev and al., 1997)	
	Biolistics (microprojectiles)	(Finer *et al.*, 1999; Hansen and Chilton, 1999; Shillito, 1999)	
	Electroporation (protoplasts)	(Fromm *et al.*, 1985; Ou-Lee *et al.*, 1986; Rhodes *et al.*, 1988; Saunders *et al.*, 1989) May be combined with liposomes (Trick and al., 1997)	
	Polyethylene glycol (PEG) treatment	(Shillito, 1999)	
	Liposomes	May be combined with electroporation (Trick and al., 1997)	
	in planta microinjection	(Leduc and al., 1996; Zhou and al., 1983)	
	Seed imbibition	(Trick and al., 1997)	
	Laser beam	(Hoffman, 1996)	
	Silicon carbide whiskers	(Thompson and al., 1995)	

Vectors often use a selectable marker to facilitate identifying those cells that have incorporated the vector. Many selectable markers are well known in the art for the use with prokaryotes, usually antibiotic-resistance genes or the use of autotrophy and

auxotrophy mutants. Table F lists often-used selectable markers for mammalian cell transfection.

Table F Useful selectable markers for eukaryote cell transfection

Selectable Marker	Selection	Action	Reference
Adenosine deaminase (ADA)	Media includes 9-β-D-xylofuranosyl adenine (Xyl-A)	Conversion of Xyl-A to Xyl-ATP, which incorporates into nucleic acids, killing cells. ADA detoxifies	(Kaufman *et al.*, 1986)
Dihydrofolate reductase (DHFR)	Methotrexate (MTX) and dialyzed serum (purine-free media)	MTX competitive inhibitor of DHFR. In absence of exogenous purines, cells require DHFR, a necessary enzyme in purine biosynthesis.	(Simonsen and Levinson, 1983)
Aminoglycoside phosphotransferase ("APH", "neo", "G418")	G418	G418, an aminoglycoside detoxified by APH, interferes with ribosomal function and consequently, translation.	(Southern and Berg, 1982)
Hygromycin-B-phosphotransferase (HPH)	hygromycin-B	Hygromycin-B, an aminocyclitol detoxified by HPH, disrupts protein translocation and promotes mistranslation.	(Palmer *et al.*, 1987)
Thymidine kinase (TK)	Forward selection (TK+): Media (HAT) incorporates aminopterin. Reverse selection (TK-): Media incorporates 5-bromodeoxyuridine (BrdU).	Forward: Aminopterin forces cells to synthesze dTTP from thymidine, a pathway requiring TK. Reverse: TK phosphorylates BrdU, which incorporates into nucleic acids, killing cells.	(Littlefield, 1964)

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce an AAP. Accordingly, the invention provides methods for producing an AAP using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding an AAP has been introduced) in a suitable medium, such that an AAP is produced. In another embodiment, the method further comprises isolating an AAP from the medium or the host cell.

Transgenic AAP animals

Transgenic animals are useful for studying the function and/or activity of an *AAP* and for identifying and/or evaluating modulators of AAP activity. "Transgenic animals" are non-human animals, preferably mammals, more preferably a rodents such as rats or mice, in which one or more of the cells include a transgene. Other transgenic animals include primates, sheep, dogs, cows, goats, chickens, amphibians, *etc.* A "transgene" is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops, and that remains in the genome of the mature animal. Transgenes preferably direct the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal with the purpose of preventing expression of a naturally encoded gene product in one or more cell types or tissues (a "knockout" transgenic animal), or serving as a marker or indicator of an integration, chromosomal location, or region of recombination (*e.g. cre/loxP* mice). A "homologous recombinant animal" is a non-human animal, such as a rodent, in which an endogenous *AAP* has been altered by an exogenous DNA molecule that recombines homologously with an endogenous *AAP* in a (*e.g.* embryonic) cell prior to development the animal. Host cells with an exogenous *AAP* can be used to produce non-human transgenic animals, such as fertilized oocytes or embryonic stem cells into which an *AAP*-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals or homologous recombinant animals.

1. *Approaches to transgenic animal production*

A transgenic animal can be created by introducing an *AAP* into the male pronuclei of a fertilized oocyte (*e.g.*, by microinjection, retroviral infection) and allowing the oocyte to develop in a pseudopregnant female foster animal (pffa). An *AAP* cDNA sequences (SEQ ID NO:1, 3, 5, 7, 9, 11, 13 or 15) can be introduced as a transgene into the genome

of a non-human animal. Alternatively, a homologue of an *AAP*, such as the naturally-occuring variant of an *AAP*, can be used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase transgene expression. Tissue-specific regulatory sequences can be operably-linked to the *AAP* transgene to direct expression of the *AAP* to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art, *e.g.* (Evans *et al.*, U.S. Patent No. 4,870,009, 1989; Hogan, 0879693843, 1994; Leder and Stewart, U.S. Patent No. 4,736,866, 1988; Wagner and Hoppe, US Patent No. 4,873,191, 1989). Other non-mice transgenic animals may be made by similar methods. A transgenic founder animal, which can be used to breed additional transgenic animals, can be identified based upon the presence of the transgene in its genome and/or expression of the transgene mRNA in tissues or cells of the animals. Transgenic animals can be bred to other transgenic animals carrying other transgenes.

2. *Vectors for transgenic animal production*

To create a homologous recombinant animal, a vector containing at least a portion of an *AAP* into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, disrupt or alter the expression of, an *AAP*. An *AAP* can be a murine gene, or other *AAP* homologue, such as a naturally occurring variant. In one approach, a knockout vector functionally disrupts an endogenous *AAP* gene upon homologous recombination, and thus a non-functional AAP protein, if any, is expressed.

Alternatively, the vector can be designed such that, upon homologous recombination, an endogenous *AAP* is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of an endogenous AAP). In this type of homologous recombination vector, the altered portion of the *AAP* is flanked at its 5'- and 3'-termini by additional nucleic acid of the *AAP* to allow for homologous recombination to occur between the exogenous *AAP* carried by the vector and an endogenous *AAP* in an embryonic stem cell. The additional flanking AAP nucleic acid is sufficient to engender homologous recombination with the endogenous *AAP*. Typically, several kilobases of flanking DNA (both at the 5'- and 3'-termini) are included in the vector (Thomas and Capecchi, 1987). The vector is then introduced into an embryonic stem cell line (*e.g.*, by electroporation), and cells in which

the introduced *AAP* has homologously-recombined with an endogenous *AAP* are selected (Li *et al.*, 1992).

3. *Introduction of an* AAP *transgene cells during development*

Selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (Bradley, 1987). A chimeric embryo can then be implanted into a suitable pffa and the embryo brought to term. Progeny harboring the homologously-recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously-recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described (Berns *et al.*, WO 93/04169, 1993; Bradley, 1991; Kucherlapati *et al.*, WO 91/01140, 1991; Le Mouellic and Brullet, WO 90/11354, 1990).

Alternatively, transgenic animals that contain selected systems that allow for regulated expression of the transgene can be produced. An example of such a system is the *cre/loxP* recombinase system of bacteriophage P1 (Lakso *et al.*, 1992). Another recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be produced as "double" transgenic animals, by mating an animal containing a transgene encoding a selected protein to another containing a transgene encoding a recombinase.

Clones of transgenic animals can also be produced (Wilmut *et al.*, 1997). In brief, a cell from a transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase. The quiescent cell can then be fused to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured to develop to a morula or blastocyte and then transferred to a pffa. The offspring borne of this female foster animal will be a clone of the "parent" transgenic animal.

Pharmaceutical compositions

The *AAP* nucleic acid molecules, AAP polypeptides, and anti-AAP Abs (active compounds) of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions. Such compositions typically

comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. A "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration (Gennaro, 2000). Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. Except when a conventional media or agent is incompatible with an active compound, use of these compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

1. *General considerations*

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration, including intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (*i.e.,* topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid (EDTA); buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The *p*H can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

2. *Injectable formulations*

Pharmaceutical compositions suitable for injection include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, CREMOPHOR EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid so as to be administered using a syringe. Such compositions should be stable during manufacture and storage and must be

preserved against contamination from microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (such as glycerol, propylene glycol, and liquid polyethylene glycol), and suitable mixtures. Proper fluidity can be maintained, for example, by using a coating such as lecithin, by maintaining the required particle size in the case of dispersion and by using surfactants. Various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, and thimerosal, can contain microorganism contamination. Isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, and sodium chloride can be included in the composition. Compositions that can delay absorption include agents such as aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, an AAP or anti-AAP antibody) in the required amount in an appropriate solvent with one or a combination of ingredients as required, followed by sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium, and the other required ingredients as discussed. Sterile powders for the preparation of sterile injectable solutions, methods of preparation include vacuum drying and freeze-drying that yield a powder containing the active ingredient and any desired ingredient from a sterile solutions.

3. *Oral compositions*

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid carrier is applied orally. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included. Tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, PRIMOGEL, or corn starch; a lubricant such as magnesium stearate or STEROTES; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

4. *Compositions for inhalation*

For administration by inhalation, the compounds are delivered as an aerosol spray from a nebulizer or a pressurized container that contains a suitable propellant, *e.g.*, a gas such as carbon dioxide.

5. *Systemic administration*

Systemic administration can also be transmucosal or transdermal. For transmucosal or transdermal administration, penetrants that can permeate the target barrier(s) are selected. Transmucosal penetrants include, detergents, bile salts, and fusidic acid derivatives. Nasal sprays or suppositories can be used for transmucosal administration. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams.

The compounds can also be prepared in the form of suppositories (*e.g.*, with bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

6. *Carriers*

In one embodiment, the active compounds are prepared with carriers that protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Such materials can be obtained commercially from ALZA Corporation (Mountain View, CA) and NOVA Pharmaceuticals, Inc. (Lake Elsinore, CA), or prepared by one of skill in the art. Liposomal suspensions can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, such as in (Eppstein *et al.*, US Patent No. 4,522,811, 1985).

7. *Unit dosage*

Oral formulations or parenteral compositions in unit dosage form can be created to facilitate administration and dosage uniformity. Unit dosage form refers to physically discrete units suited as single dosages for the subject to be treated, containing a therapeutically effective quantity of active compound in association with the required pharmaceutical carrier. The specification for the unit dosage forms of the invention are dictated by, and directly dependent on, the unique characteristics of the active compound

and the particular desired therapeutic effect, and the inherent limitations of compounding the active compound.

8. *Gene therapy compositions*

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (Nabel and Nabel, US Patent No. 5,328,470, 1994), or by stereotactic injection (Chen *et al.*, 1994). The pharmaceutical preparation of a gene therapy vector can include an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

9. *Dosage*

The pharmaceutical composition and method of the present invention may further comprise other therapeutically active compounds as noted herein that are usually applied in the treatment of the above mentioned pathological conditions.

In the treatment or prevention of conditions which require AAP modulation an appropriate dosage level will generally be about 0.01 to 500 mg per kg patient body weight per day which can be administered in single or multiple doses. Preferably, the dosage level will be about 0.1 to about 250 mg/kg per day; more preferably about 0.5 to about 100 mg/kg per day. A suitable dosage level may be about 0.01 to 250 mg/kg per day, about 0.05 to 100 mg/kg per day, or about 0.1 to 50 mg/kg per day. Within this range the dosage may be 0.05 to 0.5, 0.5 to 5 or 5 to 50 mg/kg per day. For oral administration, the compositions are preferably provided in the form of tablets containing 1.0 to 1000 milligrams of the active ingredient, particularly 1.0, 5.0, 10.0, 15.0. 20.0, 25.0, 50.0, 75.0, 100.0, 150.0, 200.0, 250.0, 300.0, 400.0, 500.0, 600.0, 750.0, 800.0, 900.0, and 1000.0 milligrams of the active ingredient for the symptomatic adjustment of the dosage to the patient to be treated. The compounds may be administered on a regimen of 1 to 4 times per day, preferably once or twice per day.

It will be understood, however, that the specific dose level and frequency of dosage for any particular patient may be varied and will depend upon a variety of factors including the activity of the specific compound employed, the metabolic stability and

length of action of that compound, the age, body weight, general health, sex, diet, mode and time of administration, rate of excretion, drug combination, the severity of the particular condition, and the host undergoing therapy.

10. *Kits for pharmaceutical compositions*

The pharmaceutical compositions can be included in a kit, container, pack, or dispenser together with instructions for administration. When the invention is supplied as a kit, the different components of the composition may be packaged in separate containers and admixed immediately before use. Such packaging of the components separately may permit long-term storage without losing the active components' functions.

Kits may also include reagents in separate containers that facilitate the execution of a specific test, such as diagnostic tests or tissue typing. For example, *AAP* DNA templates and suitable primers may be supplied for internal controls.

(a) *Containers or vessels*

The reagents included in the kits can be supplied in containers of any sort such that the life of the different components are preserved, and are not adsorbed or altered by the materials of the container. For example, sealed glass ampules may contain lyophilized luciferase or buffer that have been packaged under a neutral, non-reacting gas, such as nitrogen. Ampoules may consist of any suitable material, such as glass, organic polymers, such as polycarbonate, polystyrene, etc., ceramic, metal or any other material typically employed to hold reagents. Other examples of suitable containers include simple bottles that may be fabricated from similar substances as ampules, and envelopes, that may consist of foil-lined interiors, such as aluminum or an alloy. Other containers include test tubes, vials, flasks, bottles, syringes, or the like. Containers may have a sterile access port, such as a bottle having a stopper that can be pierced by a hypodermic injection needle. Other containers may have two compartments that are separated by a readily removable membrane that upon removal permits the components to mix. Removable membranes may be glass, plastic, rubber, etc.

(b) *Instructional materials*

Kits may also be supplied with instructional materials. Instructions may be printed on paper or other substrate, and/or may be supplied as an electronic-readable medium, such as a floppy disc, CD-ROM, DVD-ROM, Zip disc, videotape, audiotape, *etc.* Detailed instructions may not be physically associated with the kit; instead, a user

may be directed to an internet web site specified by the manufacturer or distributor of the kit, or supplied as electronic mail.

Screening and detection methods

The isolated nucleic acid molecules of the invention can be used to express an AAP (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect an *AAP* mRNA (*e.g.*, in a biological sample) or a genetic lesion in an *AAP*, and to modulate AAP activity, as described below. In addition, AAP polypeptides can be used to screen drugs or compounds that modulate the AAP activity or expression as well as to treat disorders characterized by insufficient or excessive production of an AAP or production of AAP forms that have decreased or aberrant activity compared to an AAP wild-type protein, or modulate biological function that involve an AAP. In addition, the anti-AAP Abs of the invention can be used to detect and isolate an AAP and modulate AAP activity.

1. *Screening assays*

The invention provides a method (screening assay) for identifying modalities, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, small molecules or other drugs), foods, combinations thereof, *etc.*, that effect an AAP, a stimulatory or inhibitory effect, inlcuding translation, transcription, activity or copies of the gene in cells. The invention also includes compounds identified in screening assays.

Testing for compounds that increase or decrease AAP activity are desirable. A compound may modulate an AAP activity by affecting: (1) the number of copies of the gene in the cell (amplifiers and deamplifiers); (2) increasing or decreasing transcription of an *AAP* (transcription up-regulators and down-regulators); (3) by increasing or decreasing the translation of an *AAP* mRNA into protein (translation up-regulators and down-regulators); or (4) by increasing or decreasing the activity of an AAP itself (agonists and antagonists).

(a) *effects of compounds*

To identify compounds that affect an AAP at the DNA, RNA and protein levels, cells or organisms are contacted with a candidate compound and the corresponding change in an AAP DNA, RNA or protein is assessed (Ausubel *et al.*, 1987). For DNA amplifiers and deamplifiers, the amount of an *AAP* DNA is measured, for those

compounds that are transcription up-regulators and down-regulators the amount of an *AAP* mRNA is determined; for translational up- and down-regulators, the amount of an AAP polypeptide is measured. Compounds that are agonists or antagonists may be identified by contacting cells or organisms with the compound, and then examining, for example, the model of angiogenesis *in vitro*.

In one embodiment, many assays for screening candidate or test compounds that bind to or modulate the activity of an AAP or polypeptide or biologically-active portion are available. Ttest compounds can be obtained using any of the numerous approaches in combinatorial library methods, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptides, while the other four approaches encompass peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997).

(b) *small molecules*

A "small molecule" refers to a composition that has a molecular weight of less than about 5 kD and more preferably less than about 4 kD, most preferably less than 0.6 kD. Small molecules can be, nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic or inorganic molecules. Libraries of chemical and/or biological mixtures, such as fungal, bacterial, or algal extracts, are known in the art and can be screened with any of the assays of the invention. Examples of methods for the synthesis of molecular libraries can be found in: (Carell *et al.*, 1994a; Carell *et al.*, 1994b; Cho *et al.*, 1993; DeWitt *et al.*, 1993; Gallop *et al.*, 1994; Zuckermann *et al.*, 1994).

Libraries of compounds may be presented in solution (Houghten *et al.*, 1992) or on beads (Lam *et al.*, 1991), on chips (Fodor *et al.*, 1993), bacteria, spores (Ladner *et al.*, US Patent No. 5,223,409, 1993), plasmids (Cull *et al.*, 1992) or on phage (Cwirla *et al.*, 1990; Devlin *et al.*, 1990; Felici *et al.*, 1991; Ladner *et al.*, US Patent No. 5,223,409, 1993; Scott and Smith, 1990). A cell-free assay comprises contacting an AAP or biologically-active fragment with a known compound that binds the AAP to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with the AAP, where determining the ability of the

test compound to interact with the AAP comprises determining the ability of the AAP to preferentially bind to or modulate the activity of an AAP target molecule.

(c) *cell-free assays*

The cell-free assays of the invention may be used with both soluble or a membrane-bound forms of an AAP. In the case of cell-free assays comprising the membrane-bound form, a solubilizing agent to maintain the AAP in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, TRITON® X-100 and others from the TRITON® series, THESIT®, Isotridecypoly(ethylene glycol ether)$_n$, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl) dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

(d) *immobilization of target molecules to facilitate screening*

In more than one embodiment of the assay methods, immobilizing either an AAP or its partner molecules can facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate high throughput assays. Binding of a test compound to an AAP, or interaction of an AAP with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants, such as microtiter plates, test tubes, and micro-centrifuge tubes. A fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For example, GST-AAP fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (SIGMA Chemical, St. Louis, MO) or glutathione derivatized microtiter plates that are then combined with the test compound or the test compound and either the non-adsorbed target protein or an AAP, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described. Alternatively, the complexes can be dissociated from the matrix, and the level of AAP binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in screening assays. Either an AAP or its target molecule can be immobilized using biotin-avidin or biotin-streptavidin systems. Biotinylation can be accomplished using many reagents, such as biotin-NHS (N-hydroxy-succinimide; PIERCE Chemicals, Rockford, IL), and immobilized in wells of streptavidin-coated 96 well plates (PIERCE Chemical). Alternatively, Abs reactive with an AAP or target molecules, but which do not interfere with binding of the AAP to its target molecule, can be derivatized to the wells of the plate, and unbound target or an AAP trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described for the GST-immobilized complexes, include immunodetection of complexes using Abs reactive with an AAP or its target, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the AAP or target molecule.

(e) *screens to identify modulators*

Modulators of AAP expression can be identified in a method where a cell is contacted with a candidate compound and the expression of an AAP mRNA or protein in the cell is determined. The expression level of the *AAP* mRNA or protein in the presence of the candidate compound is compared to the AAP mRNA or protein levels in the absence of the candidate compound. The candidate compound can then be identified as a modulator of the AAP mRNA or protein expression based upon this comparison. For example, when expression of an AAP mRNA or protein is greater (*i.e.*, statistically significant) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of the AAP mRNA or protein expression. Alternatively, when expression of the AAP mRNA or protein is less (statistically significant) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of the AAP mRNA or protein expression. The level of an AAP mRNA or protein expression in the cells can be determined by methods described for detecting an AAP mRNA or protein.

(i) *hybrid assays*

In yet another aspect of the invention, an AAP can be used as "bait" in two-hybrid or three hybrid assays (Bartel *et al.*, 1993; Brent *et al.*, WO94/10300, 1994; Iwabuchi *et al.*, 1993; Madura *et al.*, 1993; Saifer *et al.*, US Patent No. 5,283,317, 1994; Zervos *et al.*, 1993) to identify other proteins that bind or interact with the AAP and modulate AAP

activity. Such AAP-bps are also likely to be involved in the propagation of signals by the AAP as, for example, upstream or downstream elements of an AAP pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for an AAP is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL4). The other construct, a DNA sequence from a library of DNA sequences that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact *in vivo*, forming an AAP-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably-linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected, and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the AAP-interacting protein.

The invention further pertains to novel agents identified by the aforementioned screening assays and uses thereof for treatments as described herein.

2. *Detection assays*

Portions or fragments of an *AAP* cDNA sequences identified herein (and the complete *AAP* gene sequences) are useful in themselves. By way of non-limiting example, these sequences can be used to: (1) identify an individual from a minute biological sample (tissue typing); and (2) aid in forensic identification of a biological sample.

(a) *Tissue typing*

The AAP sequences of the invention can be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes and probed on a Southern blot to yield unique bands. The sequences of the invention are useful as additional DNA markers for "restriction fragment length polymorphisms" (RFLP; (Smulson *et al.*, US Patent No. 5,272,057, 1993)).

Furthermore, the *AAP* sequences can be used to determine the actual base-by-base DNA sequence of targeted portions of an individual's genome. *AAP* sequences can be used to prepare two PCR primers from the 5'- and 3'-termini of the sequences that can then be used to amplify an the corresponding sequences from an individual's genome and then sequence the amplified fragment.

Panels of corresponding DNA sequences from individuals can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the invention can be used to obtain such identification sequences from individuals and from tissue. The *AAP* sequences of the invention uniquely represent portions of an individual's genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. The allelic variation between individual humans occurs with a frequency of about once ever 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include RFLPs.

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in noncoding regions, fewer sequences are necessary to differentiate individuals. Noncoding sequences can positively identify individuals with a panel of 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, and 15 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive medicine

The invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to treat an individual prophylactically. Accordingly, one aspect of the invention relates to diagnostic assays for determining an AAP and/or nucleic acid expression as well as AAP activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant AAP expression or activity, including cancer. The invention also provides for prognostic (or predictive)

assays for determining whether an individual is at risk of developing a disorder associated with an AAP, nucleic acid expression or activity. For example, mutations in an *AAP* can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to prophylactically treat an individual prior to the onset of a disorder characterized by or associated with the AAP, nucleic acid expression, or biological activity.

Another aspect of the invention provides methods for determining AAP activity, or nucleic acid expression, in an individual to select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of modalities (*e.g.*, drugs, foods) for therapeutic or prophylactic treatment of an individual based on the individual's genotype (*e.g.*, the individual's genotype to determine the individual's ability to respond to a particular agent). Another aspect of the invention pertains to monitoring the influence of modalities (*e.g.*, drugs, foods) on the expression or activity of an AAP in clinical trials.

1. *Diagnostic assays*

An exemplary method for detecting the presence or absence of an AAP in a biological sample involves obtaining a biological sample from a subject and contacting the biological sample with a compound or an agent capable of detecting the AAP or the *AAP* nucleic acid (*e.g.*, mRNA, genomic DNA) such that the presence of the AAP is confirmed in the sample. An agent for detecting the *AAP* mRNA or genomic DNA is a labeled nucleic acid probe that can hybridize to the *AAP* mRNA or genomic DNA. The nucleic acid probe can be, for example, a full-length *AAP* nucleic acid, such as the nucleic acid of SEQ ID NOS: 1, 3, 5, 7, 9, 11, 13 or 15, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to an *AAP* mRNA or genomic DNA.

An agent for detecting an AAP polypeptide is an antibody capable of binding to the AAP, preferably an antibody with a detectable label. Abs can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment (*e.g.*, F_{ab} or $F(ab')_2$) can be used. A labeled probe or antibody is coupled (*i.e.*, physically linking) to a detectable substance, as well as indirect detection of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently-labeled secondary antibody and end-labeling of a

DNA probe with biotin such that it can be detected with fluorescently-labeled streptavidin. The term "biological sample" includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. The detection method of the invention can be used to detect an *AAP* mRNA, protein, or genomic DNA in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of an *AAP* mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of an AAP polypeptide include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations, and immunofluorescence. *In vitro* techniques for detection of an *AAP* genomic DNA include Southern hybridizations and fluorescence in situ hybridization (FISH). Furthermore, *in vivo* techniques for detecting an AAP include introducing into a subject a labeled anti-AAP antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample from the subject contains protein molecules, and/or mRNA molecules, and/or genomic DNA molecules. A preferred biological sample is blood.

In another embodiment, the methods further involve obtaining a biological sample from a subject to provide a control, contacting the sample with a compound or agent to detect an *AAP*, mRNA, or genomic DNA, and comparing the presence of the *AAP*, mRNA or genomic DNA in the control sample with the presence of the AAP, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting an AAP in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting an AAP or an *AAP* mRNA in a sample; reagent and/or equipment for determining the amount of an AAP in the sample; and reagent and/or equipment for comparing the amount of an AAP in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect the AAP or nucleic acid.

2. *Prognostic assays*

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with an aberrant AAP expression or activity. For example, the assays described herein, can be used to

identify a subject having or at risk of developing a disorder associated with AAP, nucleic acid expression or activity. Alternatively, the prognostic assays can be used to identify a subject having or at risk for developing a disease or disorder. Tthe invention provides a method for identifying a disease or disorder associated with an aberrant AAP expression or activity in which a test sample is obtained from a subject and the AAP or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected. A test sample is a biological sample obtained from a subject. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Pognostic assays can be used to determine whether a subject can be administered a modality (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, food, *etc.*) to treat a disease or disorder associated with an aberrant AAP expression or activity. Such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder. The invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with an aberrant AAP expression or activity in which a test sample is obtained and the AAP or nucleic acid is detected (*e.g.*, where the presence of the AAP or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with the aberrant AAP expression or activity).

The methods of the invention can also be used to detect genetic lesions in an *AAP* to determine if a subject with the genetic lesion is at risk for a disorder characterized by aberrant angiogenesis. Methods include detecting, in a sample from the subject, the presence or absence of a genetic lesion characterized by at an alteration affecting the integrity of a gene encoding an AAP polypeptide, or the mis-expression of an *AAP*. Such genetic lesions can be detected by ascertaining: (1) a deletion of one or more nucleotides from an *AAP*; (2) an addition of one or more nucleotides to an *AAP*; (3) a substitution of one or more nucleotides in an *AAP*, (4) a chromosomal rearrangement of an *AAP* gene; (5) an alteration in the level of an *AAP* mRNA transcripts, (6) aberrant modification of an *AAP*, such as a change genomic DNA methylation, (7) the presence of a non-wild-type splicing pattern of an *AAP* mRNA transcript, (8) a non-wild-type level of an *AAP*, (9) allelic loss of an *AAP*, and/or (10) inappropriate post-translational modification of an AAP polypeptide. There are a large number of known assay techniques that can be used

to detect lesions in an *AAP*. Any biological sample containing nucleated cells may be used.

In certain embodiments, lesion detection may use a probe/primer in a polymerase chain reaction (PCR) (*e.g.*, (Mullis, US Patent No. 4,683,202, 1987; Mullis *et al.*, US Patent No. 4,683,195, 1987), such as anchor PCR or rapid amplification of cDNA ends (RACE) PCR, or, alternatively, in a ligation chain reaction (LCR) (*e.g.*, (Landegren *et al.*, 1988; Nakazawa *et al.*, 1994), the latter is particularly useful for detecting point mutations in *AAP*-genes (Abravaya *et al.*, 1995). This method may include collecting a sample from a patient, isolating nucleic acids from the sample, contacting the nucleic acids with one or more primers that specifically hybridize to an *AAP* under conditions such that hybridization and amplification of the *AAP* (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990), transcriptional amplification system (Kwoh *et al.*, 1989); Qβ Replicase (Lizardi *et al.*, 1988), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules present in low abundance.

Mutations in an *AAP* from a sample can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

Hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high-density arrays containing hundreds or thousands of oligonucleotides probes, can identify genetic mutations in an *AAP* (Cronin *et al.*, 1996; Kozal *et al.*, 1996). For example, genetic mutations in an *AAP* can be identified in two-dimensional arrays containing

light-generated DNA probes as described in Cronin, *et al.*, supra. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence an *AAP* and detect mutations by comparing the sequence of the sample AAP-with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on classic techniques (Maxam and Gilbert, 1977; Sanger *et al.*, 1977). Any of a variety of automated sequencing procedures can be used when performing diagnostic assays (Naeve *et al.*, 1995) including sequencing by mass spectrometry (Cohen *et al.*, 1996; Griffin and Griffin, 1993; Koster, WO94/16101, 1994).

Other methods for detecting mutations in an *AAP* include those in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers *et al.*, 1985). In general, the technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labeled) RNA or DNA containing a wild-type *AAP* sequence with potentially mutant RNA or DNA obtained from a sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as those that arise from base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S_1 nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. The digested material is then separated by size on denaturing polyacrylamide gels to determine the mutation site (Grompe *et al.*, 1989; Saleeba and Cotton, 1993). The control DNA or RNA can be labeled for detection.

Mismatch cleavage reactions may employ one or more proteins that recognize mismatched base pairs in double-stranded DNA (DNA mismatch repair) in defined systems for detecting and mapping point mutations in an *AAP* cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.*, 1994). According to an exemplary embodiment, a probe based on a wild-type *AAP* sequence is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like (Modrich *et al.*, US Patent No. 5,459,039, 1995).

Electrophoretic mobility alterations can be used to identify mutations in an *AAP*. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Cotton, 1993; Hayashi, 1992; Orita *et al.*, 1989). Single-stranded DNA fragments of sample and control *AAP* nucleic acids are denatured and then renatured. The secondary structure of single-stranded nucleic acids varies according to sequence; the resulting alteration in electrophoretic mobility allows detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a sequence changes. The subject method may use heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.*, 1991).

The migration of mutant or wild-type fragments can be assayed using denaturing gradient gel electrophoresis (DGGE; (Myers *et al.*, 1985). In DGGE, DNA is modified to prevent complete denaturation, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. A temperature gradient may also be used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rossiter and Caskey, 1990).

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions

that permit hybridization only if a perfect match is found (Saiki *et al.*, 1986; Saiki *et al.*, 1989). Such allele-specific oligonucleotides are hybridized to PCR-amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used. Oligonucleotide primers for specific amplifications may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization (Gibbs *et al.*, 1989)) or at the extreme 3'-terminus of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prosser, 1993). Novel restriction site in the region of the mutation may be introduced to create cleavage-based detection (Gasparini *et al.*, 1992). Certain amplification may also be performed using *Taq* ligase for amplification (Barany, 1991). In such cases, ligation occurs only if there is a perfect match at the 3'-terminus of the 5' sequence, allowing detection of a known mutation by scoring for amplification.

The described methods may be performed, for example, by using pre-packaged kits comprising at least one probe (nucleic acid or antibody) that may be conveniently used, for example, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving an AAP.

Furthermore, any cell type or tissue in which an AAP is expressed may be utilized in the prognostic assays described herein.

3. *Pharmacogenomics*

Agents, or modulators that have a stimulatory or inhibitory effect on AAP activity or expression, as identified by a screening assay can be administered to individuals to treat, prophylactically or therapeutically, disorders, including those associated with angiogenesis. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between a subject's genotype and the subject's response to a foreign modality, such as a food, compound or drug) may be considered. Metabolic differences of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Pharmacogenomics can further be used to determine appropriate dosages and

therapeutic regimens. Accordingly, the activity of an AAP, expression of an *AAP* nucleic acid, or an *AAP* mutation(s) in an individual can be determined to guide the selection of appropriate agent(s) for therapeutic or prophylactic treatment.

Pharmacogenomics deals with clinically significant hereditary variations in the response to modalities due to altered modality disposition and abnormal action in affected persons (Eichelbaum and Evert, 1996; Linder *et al.*, 1997). In general, two pharmacogenetic conditions can be differentiated: (1) genetic conditions transmitted as a single factor altering the interaction of a modality with the body (altered drug action) or (2) genetic conditions transmitted as single factors altering the way the body acts on a modality (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as nucleic acid polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) explains the phenomena of some patients who show exaggerated drug response and/or serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the *CYP2D6* gene is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers due to mutant *CYP2D6* and *CYP2C19* frequently experience exaggerated drug responses and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM shows no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. At the other extreme are the so-called ultra-rapid metabolizers who are unresponsive to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

The activity of an AAP, expression of an *AAP* nucleic acid, or mutation content of an *AAP* in an individual can be determined to select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with an AAP modulator, such as a modulator identified by one of the described exemplary screening assays.

4. *Monitoring effects during clinical trials*

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of an AAP (*e.g.*, the ability to modulate angiogenesis) can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent determined by a screening assay to increase an *AAP* expression, protein levels, or up-regulate an AAP's activity can be monitored in clinical trails of subjects exhibiting decreased *AAP* expression, protein levels, or down-regulated AAP activity. Alternatively, the effectiveness of an agent determined to decrease an *AAP* expression, protein levels, or down-regulate an AAP's activity, can be monitored in clinical trails of subjects exhibiting increased the *AAP* expression, protein levels, or up-regulated AAP activity. In such clinical trials, the expression or activity of the AAP and, preferably, other genes that have been implicated in, for example, angiogenesis can be used as a "read out" or markers for a particular cell's responsiveness.

For example, genes, including an *AAP*, that are modulated in cells by treatment with a modality (*e.g.*, food, compound, drug or small molecule) can be identified. To study the effect of agents on angiogenesis, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of an *AAP* and other genes implicated in the disorder. The gene expression pattern can be quantified by Northern blot analysis, nuclear run-on or RT-PCR experiments, or by measuring the amount of protein, or by measuring the activity level of the AAP or other gene products. In this manner, the gene expression pattern itself can serve as a marker, indicative of the cellular physiological response to the agent. Accordingly, this response state may be

determined before, and at various points during, treatment of the individual with the agent.

The invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, peptidomimetic, nucleic acid, small molecule, food or other drug candidate identified by the screening assays described herein) comprising the steps of (1) obtaining a pre-administration sample from a subject; (2) detecting the level of expression of an AAP, mRNA, or genomic DNA in the preadministration sample; (3) obtaining one or more post-administration samples from the subject; (4) detecting the level of expression or activity of the AAP, mRNA, or genomic DNA in the post-administration samples; (5) comparing the level of expression or activity of the AAP, mRNA, or genomic DNA in the pre-administration sample with the AAP, mRNA, or genomic DNA in the post administration sample or samples; and (6) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of the AAP to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of the AAP to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

5. *Methods of treatment*

The invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant AAP expression or activity. Furthermore, these same methods of treatment may be used to induce or inhibit angiogenesis, by changing the level of expression or activity of an AAP.

6. *Disease and disorders*

Diseases and disorders that are characterized by increased AAP levels or biological activity may be treated with therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Antognists may be administered in a therapeutic or prophylactic manner. Therapeutics that may be used include: (1) AAP peptides, or analogs, derivatives, fragments or homologs thereof; (2) Abs to an AAP peptide; (3) *AAP* nucleic acids; (4) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences) that are used to eliminate

endogenous function of by homologous recombination (Capecchi, 1989); or (5) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or Abs specific to an AAP) that alter the interaction between an AAP and its binding partner.

Diseases and disorders that are characterized by decreased AAP levels or biological activity may be treated with therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered therapeutically or prophylactically. Therapeutics that may be used include peptides, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or *AAP* mRNAs). Methods include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, *etc.*) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, and the like).

7. *Prophylactic methods*

The invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant AAP expression or activity, by administering an agent that modulates an AAP expression or at least one AAP activity. Subjects at risk for a disease that is caused or contributed to by an aberrant AAP expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the AAP aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of AAP aberrancy, for example, an AAP agonist or AAP antagonist can be used to treat the subject. The appropriate agent can be determined based on screening assays.

8. Therapeutic methods

Another aspect of the invention pertains to methods of modulating an AAP expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of

AAP activity associated with the cell. An agent that modulates AAP activity can be a nucleic acid or a protein, a naturally occurring cognate ligand of an AAP, a peptide, an AAP peptidomimetic, or other small molecule. The agent may stimulate AAP activity. Examples of such stimulatory agents include an active AAP and an *AAP* nucleic acid molecule that has been introduced into the cell. In another embodiment, the agent inhibits AAP activity. Examples of inhibitory agents include antisense *AAP* nucleic acids and anti-AAP Abs. Modulatory methods can be performed *in vitro* (*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of an AAP or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay), or combination of agents that modulates (*e.g.*, up-regulates or down-regulates) AAP expression or activity. In another embodiment, the method involves administering an AAP or nucleic acid molecule as therapy to compensate for reduced or aberrant AAP expression or activity.

Stimulation of AAP activity is desirable in situations in which AAP is abnormally down-regulated and/or in which increased AAP activity is likely to have a beneficial effect. One example of such a situation is where a subject has a disorder characterized by aberrant angiogenesis (*e.g.*, cancer).

9. *Determination of the biological effect of the therapeutic*

Suitable *in vitro* or *in vivo* assays can be performed to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given therapeutic exerts the desired effect upon the cell type(s). Modalities for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

10. *Prophylactic and therapeutic uses of the compositions of the invention*

AAP nucleic acids and proteins are useful in potential prophylactic and therapeutic applications implicated in a variety of disorders including, but not limited to those related to angiogenesis.

As an example, a cDNA encoding an AAP may be useful in gene therapy, and the protein may be useful when administered to a subject in need thereof.

AAP nucleic acids, or fragments thereof, may also be useful in diagnostic applications, wherein the presence or amount of the nucleic acid or the protein is to be assessed. A further use could be as an anti-bacterial molecule (*i.e.*, some peptides have been found to possess anti-bacterial properties). These materials are further useful in the generation of Abs that immunospecifically bind to the novel substances of the invention for use in therapeutic or diagnostic methods.

The following example is meant to not be limiting.

EXAMPLE

Identification of genes differentially-regulated

A comprehensive mRNA profiling technique (GeneCalling) was used to determine differential gene expression profiles of human endothelial cells undergoing differentiation into tube-like structures (Kahn *et al.*, 2000). To confirm the expression data from GeneCalling, independent experiments were undertaken that used gene-specific PCR oligonucleotide primer pairs and an oligonucleotide probe labeled with a fluorescent dye at the 5' end and quencher fluorescent dye at the 3' end.. Total RNA (50 ng) was added to a 50 µl RT-PCR mixture and run.

The following data were collected:

hEF G	collagen gel 24 hr versus 4h	4.5 fold upregulated
hTRG	collagen gel 24 hr versus 4h	3.5 fold upregulated
KLP	collagen gel 24 hr versus 4h	3.5 fold upregulated
myosin X	collagen gel 24 hr versus 4h	3.5 fold upregulated
NHR	collagen gel 24 hr versus 4h	7.3 fold downregulated
HBAZF	collagen gel 24 hr versus 4h	2.1 fold upregulated

EQUIVALENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered within the scope of the following claims.

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All publications and patents mentioned in the above specification are herein incorporated by reference.